

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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Limits

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History

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Show:

☐ 1: AAA28373. Antennepedia prot...[gi:156934]

[BLink](#), [Domains](#), [Links](#)

LOCUS AAA28373 74 aa linear INV 26-APR-1993

DEFINITION Antennepedia protein.

ACCESSION AAA28373

VERSION AAA28373.1 GI:156934

DBSOURCE locus DROANTC2 accession [K01948.1](#)

KEYWORDS .

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM [Drosophila melanogaster](#)

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 .(residues 1 to 74)

AUTHORS McGinnis,W., Garber,R.L., Wirz,J., Kuroiwa,A. and Gehring,W.J.

TITLE A homologous protein-coding sequence in Drosophila homeotic genes  
and its conservation in other metazoans

JOURNAL Cell 37 (2), 403-408 (1984)

MEDLINE [84205674](#)

PUBMED [6327065](#)

COMMENT Method: conceptual translation.

FEATURES Location/Qualifiers

source

1..74

/organism="Drosophila melanogaster"

/db\_xref="taxon:7227"

/map="right arm of ch. 3"

Protein

1..74

/name="Antennepedia protein"

CDS

1..74

/coded\_by="complement(K01948.1:<1..>222)"

ORIGIN

1 iylepterkr grqtytryqt lelekefhfn ryltrrrrie iahalclter qikiwfnrr

61 mkwkkenk tk gepd

//

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[NCBI](#) | [NLM](#) | [NIH](#)

Apr 24 2003 13:08:07

>gi|156934|gb|AAA28373.1| Antennepedia protein  
Length = 74

Score = 61.7 bits (138), Expect = 1e-09  
Identities = 16/16 (100%), Positives = 16/16 (100%)

Query: 1 RQIKIWFQNRRMKWKK 16  
RQIKIWFQNRRMKWKK  
Sbjct: 50 RQIKIWFQNRRMKWKK 65

	BLAST	Protein	Structure	PubMed	Taxonomy
	Genome	Nucleotide	3D-Domains	Books	Help

Query: gi|156934 Antennapedia protein













Best hits	Common Tree	Taxonomy Report	3D structures	CDD-Search	GI list
-----------	-------------	-----------------	---------------	------------	---------

200 BLAST hits to 59 unique species [Sort by taxonomy proximity](#)

☐ Archaea
 ☐ Bacteria
 ☐ 199 Metazoa
 ☐ Fungi
 ☐ Plants
 ☐ 1 Viruses
 ☐ Other Eukaryotae

Keep only  ☒ Cut-Off

74 aa

	SCORE	P	ACCESSION	GI	PROTEIN DESCRIPTION
	362	20	<a href="#">AAC31945</a>	<a href="#">3420836</a>	Antennapedia homeotic protein [Anop
	362	19	<a href="#">BAA04087</a>	<a href="#">391615</a>	Antennapedia homologue protein [Bom
	362	35	<a href="#">A25399</a>	<a href="#">84890</a>	homeotic protein Antennapedia - fru
	362	34	<a href="#">AAO00997</a>	<a href="#">27374237</a>	Antp-PA [Drosophila erecta]
	362	20	<a href="#">EAA07256</a>	<a href="#">21295111</a>	agCP12956 [Anopheles gambiae str. P
	362	19	<a href="#">S58850</a>	<a href="#">1363994</a>	homeotic protein abd-A - Junonia co
	362	32	<a href="#">CAA43307</a>	<a href="#">829192</a>	Antp [Drosophila subobscura]
	357	31	<a href="#">AAA28737</a>	<a href="#">158023</a>	homeobox protein
	357	35	<a href="#">1HOM</a>	<a href="#">443020</a>	Chain , Antennapedia Protein (Home
	355	19	<a href="#">AAF69136</a>	<a href="#">7767519</a>	prothoraxless [Tribolium castaneum]
	355	19	<a href="#">AAK96031</a>	<a href="#">15450324</a>	homeodomain transcription factor Pr
	349	19	<a href="#">CAC06383</a>	<a href="#">9967824</a>	Antennapedia protein [Apis mellifer

GenCore version 5.1.4.p5.4578  
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OM nucleic - nucleic search, using sw model

Run on: April 19, 2003, 00:06:36 ; Search time 965 Seconds  
(without alignments)  
5971.353 Million cell updates/sec

Title: US-09-654-743-51  
Perfect score: 198  
Sequence: 1 tatgaagcagcgtcttac.....accacgggtgcaataaccta 198

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenBank:

- 1: gb.ba.\*
- 2: gb.htg.\*
- 3: gb.in.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pl.\*
- 9: gb.pr.\*
- 10: gb.ro.\*
- 11: gb.sts.\*
- 12: gb.sy.\*
- 13: gb.un.\*
- 14: gb.vi.\*
- 15: em.ba.\*
- 16: em.fun.\*
- 17: em.hum.\*
- 18: em.in.\*
- 19: em.mu.\*
- 20: em.om.\*
- 21: em.or.\*
- 22: em.ov.\*
- 23: em.pat.\*
- 24: em.ph.\*
- 25: em.pl.\*
- 26: em.ro.\*
- 27: em.sts.\*
- 28: em.un.\*
- 29: em.vi.\*
- 30: em.htg\_hum.\*
- 31: em.htg\_inv.\*
- 32: em.htg\_other.\*
- 33: em.htg\_mus.\*
- 34: em.htg\_pln.\*
- 35: em.htg\_rod.\*
- 36: em.htg\_mam.\*
- 37: em.htg\_vrt.\*
- 38: em.sy.\*
- 39: em.htgo\_hum.\*
- 40: em.htgo\_mus.\*
- 41: em.htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	198	100.0	2100	6	AX412124 Sequence
2	194.8	98.4	2691	6	AR106400 Sequence
3	194.8	98.4	2691	6	AR116702 Sequence
4	194.8	98.4	2691	10	MMU88990 Mus musculus
5	186.8	94.3	1988	10	MMU36842 Mus musculus
6	182	91.9	1491	10	AF183429 Rattus no
7	182	91.9	2468	10	AB033366 Rattus no
8	182	91.9	2032	10	AF304334 Rattus no
9	180.4	91.1	2032	10	AF304333 Rattus no
10	173	87.4	1659	6	E31042 Method for
11	173	87.4	1659	9	U32974 Human IAP-1
12	173	87.4	2086	9	BC032729 Homo sapi
13	173	87.4	2404	6	AX429575 Sequence
14	173	87.4	2540	6	AR103281 Sequence
15	173	87.4	2540	6	AX412118 Sequence
16	173	87.4	2540	9	HSU45880 Human X-lin
17	173	87.4	3000	6	AX412131 Sequence
18	173	87.4	5232	6	AR106397 Sequence
19	173	87.4	5232	6	AR116699 Sequence
20	157	79.3	1752	6	AX104956 Sequence
21	157	79.3	1752	9	AF164681 Homo sapi
22	157	79.3	154214	9	AC079753 Homo sapi
23	149	75.3	1758	6	AX370787 Sequence
24	149	75.3	1758	6	AX370789 Sequence
25	149	75.3	4993	6	AX104968 Sequence
26	149	75.3	4993	9	AF164682 Homo sapi
27	149	75.3	144301	9	AC010467 Homo sapi
28	149	75.3	165662	9	AC092070 Homo sapi
29	147.4	74.4	711	6	AR121220 Sequence
30	147.4	74.4	711	6	AR123871 Sequence
31	147.4	74.4	2032	9	AF420440 Homo sapi
32	145.8	73.6	711	9	AY030052 Sequence
33	145.8	73.6	711	9	AY030052 Sequence
34	144.2	72.8	711	9	AY030053 Gorilla g
35	144.2	72.8	711	9	AY030053 Gorilla g
36	131.6	66.5	187568	9	AP002967 Homo sapi
37	130	65.7	184439	2	AP003085 Homo sapi
38	121.4	61.3	327	4	AF458770 Bos taurus
39	104.2	52.6	1740	5	AF451854 Gallus ga
40	85.8	43.3	133391	9	HSJ315G1 Human DNA
41	85.8	43.3	201197	2	HS424J12 Human DNA
42	77	38.9	1550	4	SSU79142 Sus scrofa
43	76.6	38.7	158093	9	AL390123 Human DNA
44	76	38.4	2563	9	HUMSCFB Homo sapien
45	76	38.4	2601	6	AR129833 Sequence

## ALIGNMENTS

RESULT 1	AX412124	Sequence 224 from Patent WO0226968.	2100 bp	DNA	linear	RAT 15-JUN-2002
LOCUS	AX412124					
DEFINITION	Sequence 224 from Patent WO0226968.					
ACCESSION	AX412124					
VERSION	AX412124.1	GI:21444584				
KEYWORDS	house mouse					
SOURCE	house mouse					
ORGANISM	Mus musculus					
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
TITLE	Korneluk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.					
JOURNAL	Antisense lrp nucleic acids and uses thereof					
	Patent: WO 0226968-A 224 04-APR-2002;					

University of Ottawa (CA) : Aegera Therapeutics Inc. (CA)

FEATURES  
source  
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/organism="Mus musculus"  
/db\_xref="taxon:10090"

BASE COUNT 615 a 417 c 482 g 586 t  
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Best Local Similarity 100.0%; Pred. No. 7.1e-46;  
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120  
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Db 976 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 1035  
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QY 121 GGAGGGCTCAGGATTTGGAAGCAAGTGAAGACCCCTGGACAGCATGCTAAGTCTCTAC 180  
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Db 1036 GGAGGGCTCAGGATTTGGAAGCAAGTGAAGACCCCTGGACAGCATGCTAAGTCTCTAC 1095  
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QY 181 CCAGGGTGCAAAATACCTA 198  
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Db 1096 CCAGGGTGCAAAATACCTA 1113  
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RESULT 2  
AR106400  
LOCUS AR106400 2691 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 9 from patent US 6107041.  
ACCESSION AR106400  
VERSION AR106400.1 GI:12820930  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2691)  
AUTHORS Korneluk, R.G., Mackenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and Pratt, C.  
TITLE Detection and modulation of IAPs for the diagnosis and treatment of proliferative disease  
JOURNAL Patent: US 6107041-A 9 22-AUG-2000;  
FEATURES Location/Qualifiers  
source 1..2691  
/organism="unknown"  
BASE COUNT 819 a 479 c 562 g 831 t  
ORIGIN

Query Match 98.4%; Score 194.8; DB 6; Length 2691;  
Best Local Similarity 99.0%; Pred. No. 5.5e-45;  
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAGCAGCGATCGTTTACTTTTGGACATGATATCTACTGTTAAACAGGAGCAGCTT 60  
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Db 1461 TATGAGCAGCGATCGTTTACTTTTGGACATGATATCTACTGTTAAACAGGAGCAGCTT 1520  
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QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120  
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Db 1521 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 1580  
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QY 121 GGAGGGCTCAGGATTTGGAAGCAAGTGAAGACCCCTGGACAGCATGCTAAGTCTCTAC 180  
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Db 1581 GGAGGGCTCAGGATTTGGAAGCAAGTGAAGACCCCTGGACAGCATGCTAAGTCTCTAC 1640  
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QY 181 CCAGGGTGCAAAATACCTA 198  
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Db 1641 CCAGGGTGCAAAATACCTA 1658  
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RESULT 3  
AR106400  
LOCUS AR106400 2691 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 9 from patent US 613437.  
ACCESSION AR106400  
VERSION AR106400.1 GI:14097024  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2691)  
AUTHORS Korneluk, R.G., Mackenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and Pratt, C.  
TITLE Modulation of IAPs for the treatment of proliferative diseases  
JOURNAL Patent: US 613437-A 9 17-OCT-2000;  
FEATURES Location/Qualifiers  
source 1..2691  
/organism="unknown"  
BASE COUNT 819 a 479 c 562 g 831 t  
ORIGIN

Query Match 98.4%; Score 194.8; DB 6; Length 2691;  
Best Local Similarity 99.0%; Pred. No. 5.5e-45;  
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 181 CCAGGGTGCAAAATACCTA 198  
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Db 1641 CCAGGGTGCAAAATACCTA 1658  
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RESULT 4  
MMU88990  
LOCUS MMU88990 2691 bp mRNA linear ROD 31-MAY-1997  
DEFINITION Mus musculus X-linked inhibitor of apoptosis (miap-3) mRNA, complete cds.  
ACCESSION U88990  
VERSION U88990.1 GI:2138318  
KEYWORDS  
SOURCE Mus musculus.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 2691)  
AUTHORS Farahani, R., Lefebvre, C., Korneluk, R.G. and Mackenzie, A.E.  
TITLE Genomic Organization and Primary Characterization of miap-3: The Murine Homologue of Human X-Linked IAP  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 2691)  
AUTHORS Farahani, R., Lefebvre, C., Korneluk, R.G. and Mackenzie, A.E.  
TITLE Direct Submission  
JOURNAL Submitted (07-FEB-1997) Molecular Genetics, Children's Hospital of Eastern Ontario, 401 Smyth Rd., Ottawa, Ontario K1H 8L1, Canada  
FEATURES Location/Qualifiers  
source 1..2691  
/organism="Mus musculus"  
/db\_xref="taxon:10090"  
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/dev\_stage="embryo"  
gene 1..2691  
exon <1..1545

AR116702  
LOCUS AR116702 2691 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 9 from patent US 613437.  
ACCESSION AR116702  
VERSION AR116702.1 GI:14097024  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2691)  
AUTHORS Korneluk, R.G., Mackenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and Pratt, C.  
TITLE Modulation of IAPs for the treatment of proliferative diseases  
JOURNAL Patent: US 613437-A 9 17-OCT-2000;  
FEATURES Location/Qualifiers  
source 1..2691  
/organism="unknown"  
BASE COUNT 819 a 479 c 562 g 831 t  
ORIGIN

Query Match 98.4%; Score 194.8; DB 6; Length 2691;  
Best Local Similarity 99.0%; Pred. No. 5.5e-45;  
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAGCAGCGATCGTTTACTTTTGGACATGATATCTACTGTTAAACAGGAGCAGCTT 60  
|||||  
Db 1461 TATGAGCAGCGATCGTTTACTTTTGGACATGATATCTACTGTTAAACAGGAGCAGCTT 1520  
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QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120  
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QY 121 GGAGGGCTCAGGATTTGGAAGCAAGTGAAGACCCCTGGACAGCATGCTAAGTCTCTAC 180  
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Db 1581 GGAGGGCTCAGGATTTGGAAGCAAGTGAAGACCCCTGGACAGCATGCTAAGTCTCTAC 1640  
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QY 181 CCAGGGTGCAAAATACCTA 198  
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Db 1641 CCAGGGTGCAAAATACCTA 1658  
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RESULT 4  
MMU88990  
LOCUS MMU88990 2691 bp mRNA linear ROD 31-MAY-1997  
DEFINITION Mus musculus X-linked inhibitor of apoptosis (miap-3) mRNA, complete cds.  
ACCESSION U88990  
VERSION U88990.1 GI:2138318  
KEYWORDS  
SOURCE Mus musculus.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 2691)  
AUTHORS Farahani, R., Lefebvre, C., Korneluk, R.G. and Mackenzie, A.E.  
TITLE Genomic Organization and Primary Characterization of miap-3: The Murine Homologue of Human X-Linked IAP  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 2691)  
AUTHORS Farahani, R., Lefebvre, C., Korneluk, R.G. and Mackenzie, A.E.  
TITLE Direct Submission  
JOURNAL Submitted (07-FEB-1997) Molecular Genetics, Children's Hospital of Eastern Ontario, 401 Smyth Rd., Ottawa, Ontario K1H 8L1, Canada  
FEATURES Location/Qualifiers  
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gene 1..2691  
exon <1..1545

JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 93 (10), 4974-4978 (1996)
MEDLINE	96209843
PUBMED	8643514
REFERENCE	2 (bases 1 to 1988)
AUTHORS	Vaux, D.L., Uren, A.G. and Pakusch, M.
TITLE	Direct Submission
JOURNAL	Submitted (21-SEP-1995) M. Pakusch, The Walter and Eliza Hall Institute, Royal Parade, Parkville, Victoria 3050, Australia
FEATURES	Location/Qualifiers
source	1. 1988
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	/tissue_type="liver"
	/dev_stage="6-8 weeks old"
gene	1. 1988
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CDS	212..1702
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	EHRRHFPNCFVLGRNVNVRSESGVSDRNFPNSTSPRNPAAEYEAIVTFGTWTS
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QY	121 GGAGGGCTCACGGATTGGAGCCAAAGTGAAGACCCCTGGGACCATGCTGAAGTGCCTAC 180
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QY	181 CCAGGGTGCAAAATACCTA 198
Db	1181 CCAGGGTGCAAAATACCTA 1198
RESULT 6	
AF183429	

LOCUS AF183429 1491 bp mRNA linear ROD 16-JUL-2002  
DEFINITION Rattus norvegicus inhibitor of apoptosis protein 3 mRNA, complete cds.  
ACCESSION AF183429  
VERSION AF183429.1 GI:10765280  
KEYWORDS Norway rat.  
SOURCE Rattus norvegicus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
REFERENCE 1 (bases 1 to 1491)  
AUTHORS Holcik.M., Lefebvre.C.A., Hicks.K. and Korneluk.R.G.  
TITLE Cloning and characterization of the rat homologues of the Inhibitor of Apoptosis protein 1, 2, and 3 genes  
JOURNAL BMC Genomics 3 (1), 5 (2002)  
PUBMED 11860601  
REFERENCE 2 (bases 1 to 1491)  
AUTHORS Holcik.M., Lefebvre.C.A., Hicks.K. and Korneluk.R.G.  
TITLE Direct Submission  
JOURNAL Submitted (08-SEP-1999) Department of Biochemistry, Microbiology and Immunology, University of Ottawa, 451 Smyth Road, Ottawa, Ontario K1H 8M5, Canada  
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source  
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/codon\_start=1  
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Matches 188; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
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Db 910 GGAGGCTCACGATTTGGAAGCCCAAGTGAAGCCCTGGGACCAAGCATGCTAGTCTAC 180  
QY 181 CCAGGCTGCAAAATACCTA 198  
Db 970 CCAGGCTGTAATATCTA 987  
RESULT 7  
AB033366  
LOCUS AB033366 2468 bp mRNA linear ROD 15-OCT-1999  
DEFINITION Rattus norvegicus riap3 mRNA, complete cds.  
ACCESSION AB033366  
VERSION AB033366.1 GI:6045147  
KEYWORDS RIAP3.

SOURCE Rattus norvegicus cdna to mRNA.  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
REFERENCE 1 (bases 1 to 2468)  
AUTHORS Saito.N.  
TITLE Rattus norvegicus X-linked inhibitor of apoptosis (riap3) mRNA  
JOURNAL Published Only in Database (1999)  
REFERENCE 2 (bases 1 to 2468)  
AUTHORS Saito.N.  
TITLE Direct Submission  
JOURNAL Submitted (07-OCT-1999) Nobuhito Saito, University of Tokyo, Department of Neurosurgery; 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-8655, Japan (E-mail:nsaito-tky@umin.ac.jp, Tel:+81-3-5800-8853, Fax:+81-3-5800-8855)  
FEATURES  
Location/Qualifiers  
1..2468  
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QY 121 GGAGGCTCACGATTTGGAAGCCCAAGTGAAGCCCTGGGACCAAGCATGCTAGTCTAC 180  
Db 1239 GGAGGCTCACGATTTGGAAGCCCAAGTGAAGCCCTGGGACCAAGCATGCTAGTCTAC 1298  
QY 181 CCAGGCTGCAAAATACCTA 198  
Db 1299 CCAGGCTGTAATATCTA 1316  
RESULT 8  
AF304334  
LOCUS AF304334 3032 bp mRNA linear ROD 19-DEC-2000  
DEFINITION Rattus norvegicus clone 2 inhibitor of apoptosis protein 3 mRNA, complete cds.  
ACCESSION AF304334  
VERSION AF304334.1 GI:11890720  
KEYWORDS Rattus norvegicus.  
SOURCE Rattus norvegicus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;







cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: National Institutes of Health Intramural  
 Sequencing Center (NISC),  
 Gaithersburg, Maryland;  
 Contact: nisc.mcgenhri.nih.gov  
 Web site: http://www.nisc.nih.gov/  
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,  
 Dietrich, N.L., Granice, S., Guan, X., Gupta, J., Haghighi, P.,  
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,  
 Maduro, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,  
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,  
 Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,  
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
 Series: IRAK Name: 69 Row: j Column: 18  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 4502142.

# FEATURES

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 YSVNKLQALAGFYALGEGDKVKCFHCGGLTDKWPSEDPWEQAKWPGCKYLLDQK  
 GQYINNIHLTHSLRECLVLTETKPTSLTRIDDTIFONPMVOEARIMGFSFKDKIKI  
 MEKIOISGNSVKSLEVLADLVNAOKDSQDSSOTSLOKELSTEQRLRLQELKLC  
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Query Match 87.4%; Score 173; DB 9; Length 2086;  
 Best Local Similarity 92.4%; Pred. No. 9.1e-39;  
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 QY 1 TATGAACACGGATCGTTACTTTTGGAACTAGGATATCTACTAGTAAAGGACGCTT 60  
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 QY 181 CCAGGGTGCAAAATACCT 197  
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Query Match 87.4%; Score 173; DB 9; Length 2086;  
 Best Local Similarity 92.4%; Pred. No. 9.1e-39;  
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 LOCUS  
 DEFINITION  
 Sequence 38 from Patent WO0226820.  
 2404 bp DNA linear PAT 21-JUN-2002

ACCESSION AX429575  
 VERSION AX429575.1 GI:21540833

# KEYWORDS

## SOURCE

human.  
 Homo sapiens

REFERENCE 1

AUTHORS Cohen, D., Dengler, U.J., Finelli, A.L., Freuler, F., Konsolaki, M.,

Reinhardt, M.W. and Zusman, S.

Titransgenic drosophila melanogaster expressing beta amyloid

Patent: WO 0226820-A 38 04-APR-2002;

NOVARTIS REFINO VERWALT GMBH (AT)

FEATURES Location/Qualifiers

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BASE COUNT 759 a 372 c 525 g 748 t

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QY 181 CCAGGGTGCAAAATACCT 197  
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LOCUS AR103281

DEFINITION Sequence 1 from patent US 6087173.

ACCESSION AR103281

VERSION AR103281.1 GI:12814869

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2540)

AUTHORS Bennett, C. Frank., Ackermann, E.J. and Cowser, L.M.

Titransgenic modulation of X-linked inhibitor of apoptosis expression

Patent: US 6087173-A 11-JUL-2000;

FEATURES Location/Qualifiers

1..2540

source /organism="unknown"

BASE COUNT 781 a 415 c 571 g 773 t

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LOCUS AX412118 2540 bp DNA linear PAT 14-JUN-2002  
DEFINITION Sequence 218 from Patent WO0226968.  
ACCESSION AX412118  
VERSION AX412118.1 GI:21444581  
KEYWORDS  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.  
TITLE Antisense lap nucleic acids and uses thereof  
JOURNAL Patent: WO 0226968-A 218 04-APR-2002;  
University of Ottawa (CA); Aegera Therapeutics Inc. (CA)

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Best Local Similarity 92.4%; Pred. No. 8.8e-39;  
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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Job time : 974 secs

GenCore version 5.1.4.p5.4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2003, 00:03:06 ; Search time 150 seconds

(without alignments)  
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Title: US-09-654-743-51

Perfect score: 198

Sequence: 1 tatgaagcacggtacgttac.....accagggtgcaataccta 198

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Result No.	Score	Query Match	Length	ID	Description
1	198	100.0	2100	18 AAT70839	Mouse apoptosis in
2	198	100.0	2100	24 ABK93872	Mouse cDNA encoding
3	194.8	98.4	2691	19 AAV55041	Murine XIAP coding
4	186.8	94.3	1988	18 AAT72710	Mouse inhibitor of
5	173	87.4	1659	21 AAZ48862	Human XIAP coding
6	173	87.4	2404	24 AAK99405	DNA of APP related
7	173	87.4	2540	18 AAT70836	Human apoptosis in
8	173	87.4	2540	21 AAA64901	Human X-linked inh
9	173	87.4	2540	24 ABK93869	Human cDNA encoding

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

10	173	87.4	3000	24 ABK93875	Human cDNA encoding
11	173	87.4	5232	19 AAV55038	Human XIAP coding
12	157	79.3	1752	22 AAD03575	Human IAP-like pro
13	149	75.3	1758	24 ABK14677	Human inhibitor of
14	149	75.3	1758	24 ABK14678	Human inhibitor of
15	149	75.3	4993	22 AAD03581	Human IAP-like pro
16	147.4	74.4	711	21 AAO06940	DNA encoding human
17	147.4	74.4	1559	24 ABK13197	Human testes speci
18	145.8	72.8	711	22 AAD03582	Chimpanzee IAP-lik
19	144.2	72.8	711	22 AAD03583	Gorilla IAP-like p
20	134.4	67.9	578	20 AAX02960	Human IL-1ra BAC c
21	109.6	55.4	802	20 AAX03018	Human IL-1ra BAC c
22	79.8	40.3	1402	20 AAX03028	Human IL-1ra BAC c
23	77.8	39.3	302	24 ABO58785	Human colon cancer
24	76	38.4	2601	18 AAT61591	Human c-IAP2. Hom
25	76	38.4	2666	18 AAT70837	Human apoptosis in
26	76	38.4	2676	24 ABK93870	Human cDNA encoding
27	76	38.4	3076	18 AAT72712	Human inhibitor of
28	76	38.4	3076	20 AAZ41005	Human cellular inh
29	76	38.4	3076	20 AAZ22096	Human cellular inh
30	76	38.4	3076	24 ABL62746	Breast cancer rela
31	76	38.4	3076	24 ABL66325	Lung cancer relate
32	76	38.4	3734	22 AAC90972	Human API2-MLT chl
33	76	38.4	3734	24 ABK52387	DNA encoding cysti
34	76	38.4	6669	19 AAV55039	Human XIAP-1 codin
35	76	38.4	6669	24 ABK93876	Human cDNA encoding
36	68	34.3	2474	24 ABK93873	Mouse cDNA encoding
37	68	34.3	2676	19 AAV55042	Murine XIAP-1 codi
38	66.4	33.5	2474	18 AAT70840	Mouse apoptosis in
39	66	33.3	7990	24 ABL54307	Chemically treated
40	66	33.3	7990	24 ABL32158	Human immune syste
41	65.8	33.2	1435	17 AAT43709	Human inhibitor of
42	65.8	33.2	2580	18 AAT70838	Human apoptosis in
43	65.8	33.2	2580	24 ABK93871	Human cDNA encoding
44	65.8	33.2	2589	18 AAT61590	Human c-IAP1. Hom
45	65.8	33.2	3532	18 AAT72711	Human inhibitor of

# ALIGNMENTS

RESULT 1	
AAT70839	
ID AAT70839 standard; cDNA; 2100 BP.	
XX AC AAT70839;	
XX DT 02-SEP-1997 (first entry)	
XX DE Mouse apoptosis inhibitor m-xiap cDNA.	
XX KW Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;	
XX KW M-XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;	
XX KW ischaemia; myocardial infarction; stroke;	
XX KW reperfusion injury; toxin-induced liver disease; gene therapy;	
XX KW diagnosis; ds.	
XX OS Mus sp.	
XX FH Key	Location/Qualifiers
XX FT CDS	127..1617
XX FT /tag= a	
XX PN MO9706255-A2.	
XX PD 20-FEB-1997.	
XX PP 05-AUG-1996;	96WO-IB01022.
XX PR 22-DEC-1995;	95US-0576956.
XX PR 04-AUG-1995;	95US-0511485.
XX PA (UYOT-) UNIV OTTAWA.	



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FT CDS 672..2162
FT /*tag= a
FT /product= XIAP
XX WO9835693-A2.
XX 20-AUG-1998.
XX 13-FEB-1998; 98WO-IB00781.
XX 13-FEB-1997; 97US-0800929.
XX (UYOT-) UNIV OTTAWA.
XX Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
XX Tsang B;
XX WPI; 1998-467164/40.
XX P-PSDB; AAW69297.
XX Inducing apoptosis in proliferative mammalian cells with inhibitor
XX of IAP or NAIP polypeptide - also methods for prognosis based on
XX presence of IAP and NAIP, specifically applied to cancers involving
XX p53 mutations
XX Claim 13; Fig 4; 147pp; English.
XX This sequence encodes the mouse XIAP protein, which is a inhibitor of
XX apoptosis protein (IAP), and can be used in the method of the invention.
XX The method is for enhancing apoptosis in cells from a mammal with
XX proliferative disease by treatment with a compound that inhibits
XX biological activity of an IAP or NAIP polypeptide. The inhibitory
XX compounds are used to treat proliferative diseases, specially cancers of
XX ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
XX liver, nasopharynx, thyroid, central nervous system, prostate, colon,
XX rectum, cervix or endometrium, particularly to increase their sensitivity
XX to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
XX detected in many cancers and are associated with poor prognosis,
XX resistance to chemotherapeutic agents and mutations in p53 (it is
XX suggested that wild-type p53 suppresses transcription of the IAP or NAIP
XX genes). Transgenic animals are used for testing the effects of antisense
XX oligonucleotides and for screening for the inhibitors.
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XX Query Match 98.4%; Score 194.8; DB 19; Length 2691;
XX Best Local Similarity 99.0%; Pred. No. 1.9e-57;
XX Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 121 GGAGGGCTCAGGATTTGGAGCCAAAGTGAAGCCCTGGGACCATGCTTAAGTGTCTAC 180
DB 1581 GGAGGGCTCAGGATTTGGAGCCAAAGTGAAGCCCTGGGACCATGCTTAAGTGTCTAC 1640
QY 181 CCAGGGTGCAAAATACCTA 198
DB 1641 CCAGGGTGCAAAATACCTA 1658
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XX RESULT 4
XX AAT72710
XX ID AAT72710 standard; DNA; 1988 BP.
XX AC AAT72710;
XX XX
XX DT 16-SEP-1997 (first entry)

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XX Mouse inhibitor of apoptosis protein homologue MIHA DNA.
XX DE
XX Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHA;
XX KW degenerative disease; infectious disease; autoimmune disease;
XX KW cancer; gene therapy; diagnosis; ss.
XX OS Mus musculus.
XX XX
XX Key Location/Qualifiers
XX CDS 212..1702
XX /*tag= a
XX
XX WO9723501-A1.
XX 03-JUL-1997.
XX XX
XX 20-DEC-1996; 96WO-AU00827.
XX XX
XX 22-DEC-1995; 95AU-0007275.
XX XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX XX
XX Vaux DL;
XX PI
XX WPI; 1997-350966/32.
XX DR P-PSDB; AAW19745.
XX DR
XX Isolated protein homologues of viral inhibitors of apoptosis - used
XX PT to modulate apoptosis for treatment of degenerative, infectious or
XX PT autoimmune diseases and cancer
XX XX
XX Claim 24; Page 44-47; 136pp; English.
XX XX
XX An isolated nucleic acid molecule (AAT72710) codes for mammalian IAP
XX homologue A (MIHA) (AAW19745), a murine homologue of baculovirus
XX inhibitor of apoptosis protein (IAP). It was isolated from a mouse
XX liver cDNA library on the basis of homology to Orgyia pseudotsugata
XX polyhedrosis virus IAP BIR and RING finger amino acid motifs.
XX CC Animal IAP homologue nucleic acids (see also AAT72711-17) can be used
XX CC to produce polypeptides useful in methods for modulating apoptosis
XX CC in animal cells, specifically for treatment, by inhibition, of
XX CC degenerative and infectious disease or, by promotion, of cancer and
XX CC autoimmune disease, and can be used for gene therapy of these
XX CC diseases.
XX XX
XX Sequence 1988 BP; 605 A; 367 C; 459 G; 557 T; 0 other;
XX
XX Query Match 94.3%; Score 186.8; DB 18; Length 1988;
XX Best Local Similarity 96.5%; Pred. No. 1e-54;
XX Matches 191; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
XX
QY 1 TATGAACACGATCGTTACTTTTGGAAACATGGATATACCTCAGTTAAACAGGAGCAGCTT 60
DB 1001 TATGAACACGATCGTTACTTTTGGAAACATGGATATACCTCAGTTAAACAGGAGCAGCTT 1060
QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120
DB 1061 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 1120
QY 121 GGAGGGCTCAGGATTTGGAAAGCCCAAGTGAAGCCCTGGGACCATGCTTAAGTGTCTAC 180
DB 1121 GGAGGGCTCAGGATTTGGAAAGCCCAAGTGAAGCCCTGGGACCATGCTTAAGTGTCTAC 1180
QY 181 CCAGGGTGCAAAATACCTA 198
DB 1181 CCAGGGTGCAAAATACCTA 1198
XX
XX RESULT 5
XX AAZ48862
XX ID AAZ48862 standard; cDNA; 1659 BP.
XX XX

```

AC AAZ48862;  
 XX 24-MAR-2000 (first entry)  
 DT Human XIAP coding sequence.  
 XX  
 DE Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;  
 XX transforming growth factor-beta activated kinase 1; monocyte migration;  
 KW TAK1 binding protein 1; extracellular matrix protein production;  
 KW cell growth inhibitor; beta-amyloid protein deposition;  
 KW immunosuppression; Transforming growth factor-beta; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX JP11326328-A.  
 XX 26-NOV-1999.  
 XX 13-MAY-1998; 98JP-0130378.  
 XX 13-MAY-1998; 98JP-0130378.  
 XX (MATSU) MATSUMOTO K.  
 XX WPI; 2000-078337/07.  
 XX P-PSDB; AAY59451.  
 XX Screening a substance which inhibits combination of the X-linked  
 XX inhibitor of apoptosis protein  
 XX Disclosure; Page 28-30; 43pp; Japanese.  
 XX This sequence encodes the human XIAP protein.  
 XX The invention relates to a method for screening a substance inhibiting  
 XX the formation of a complex between XIAP and TAB1, in which X-linked  
 XX inhibitor of apoptosis protein (XIAP), transforming growth factor-beta  
 XX activated kinase 1(TAK1) binding protein 1(TAB1) and a substance to be  
 XX tested are contacted with each other and then the presence or formation  
 XX of a complex between XIAP and TAB1 is detected. The substance or formation  
 XX as a drug for extracellular matrix protein production enhancement, cell  
 XX growth inhibition, monocyte migration, physiologically active substance  
 XX induction, immunosuppression, and beta-amyloid protein deposition. A  
 XX substance inhibiting the formation of a complex between TAB1 and XIAP as  
 XX well as between XIAP and TGF-beta (Transforming growth factor-beta) type  
 XX I and/or type II receptor is useful as a drug.

Query Match 87.4%; Score 173; DB 21; Length 1659;  
 Best Local Similarity 92.4%; Pred. No. 6.3e-50;  
 Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 TATGAGCAGCGATCGTTACTTTTGGACATGATATACTAGTTAAACAAGGAGCAGCTT 60  
 DB 874 TATGAGCAGCGATCGTTACTTTTGGACATGATATACTAGTTAAACAAGGAGCAGCTT 933  
 QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATGAAGTGAAGTGTTCACCTGTGA 120  
 DB 934 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATGAAGTGAAGTGTTCACCTGTGA 993  
 QY 121 GGAGGCTCACGATTTGAAGCAAGTGAAGACCCCTGGGACCGATGCTTAAGTGTAC 180  
 DB 994 GGAGGCTAACCTGATTTGAAGCCAGTGAAGCCCTGGGACCGATGCTTAAGTGTAC 1053  
 QY 181 CCAGGCTGCAATACCT 197  
 DB 1054 CCAGGCTGCAATATCT 1070

RESULT 6  
 ID AAK99405  
 XX AAK99405 standard; DNA; 2404 BP.

AC AAK99405;  
 XX 27-JUN-2002 (first entry)  
 DT DNA of APP related human homologue hCP35211.  
 DE  
 XX Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta;  
 KW amyloid precursor protein; tissue-specific expression control; human APP;  
 KW APP pathway modulator; gene therapy; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 XX CDS 692..1528  
 XX /\*tag- a  
 XX /product= "Protein of human homologue hCP35211"  
 XX /note= "No start codon"  
 XX  
 XX W0200226820-A2.  
 XX 04-APR-2002.  
 XX 01-OCT-2001; 2001WO-EP11345.  
 XX 29-SEP-2000; 2000US-236893P.  
 XX 14-JUN-2001; 2001US-298309P.  
 XX (NOVS ) NOVARTIS AG  
 XX (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
 XX Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;  
 XX Reinhardt MWHM, Zusman S;  
 XX WPI; 2002-315796/35.  
 XX P-PSDB; RAO20511.  
 XX New transgenic fly, containing DNA encoding an Abeta portion of human  
 XX APP, useful for identifying agents which modulate the APP pathway and  
 XX which can be used to treat Alzheimer's disease.  
 XX Example 4; Page 111; 129pp; English.  
 XX The invention relates to a transgenic fly whose genome comprises DNA  
 XX encoding a polypeptide having the Abeta portion of human amyloid  
 XX precursor protein (APP), fused to a signal sequence. The DNA sequence  
 XX encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in  
 XX the specification. The DNA sequence is operably linked to a tissue-  
 XX specific expression control sequence. Expression of the sequence gives  
 XX the fly an altered phenotype. The purpose of the invention is for  
 XX identifying agents that inhibit or promote the expression and/or function  
 XX of genes or encoded polypeptides which modify the APP pathway. The agent  
 XX is a compound, triple helix DNA, antisense oligonucleotide, double  
 XX stranded RNA molecule, ribozyme, or particularly an antibody. It is used  
 XX to treat conditions such as Alzheimer's disease. The agent can be used as  
 XX an APP pathway modulator or in gene therapy. This polynucleotide sequence  
 XX represents the DNA of the APP related human homologue hCP35211.  
 XX Sequence 2404 BP; 759 A; 372 C; 525 G; 748 T; 0 other;  
 Query Match 87.4%; Score 173; DB 24; Length 2404;  
 Best Local Similarity 92.4%; Pred. No. 7.3e-50;  
 Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
 QY 1 TATGAGCAGCGATCGTTACTTTTGGACATGATATACTAGTTAAACAAGGAGCAGCTT 60  
 DB 827 TATGAGCAGCGATCGTTACTTTTGGACATGATATACTAGTTAAACAAGGAGCAGCTT 886  
 QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATGAAGTGAAGTGTTCACCTGTGA 120  
 DB 887 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATGAAGTGAAGTGTTCACCTGTGA 946  
 QY 121 GGAGGCTCACGATTTGAAGCAAGTGAAGACCCCTGGGACCGATGCTTAAGTGTAC 180

Db 947 GGAGGGCTAACTGATTGGAGCCAGTGGAACCCCTGGGAACAACATGCTAAATGGTAT 1006

QY 181 CCAGGGTGCAAATACCT 197  
 Db 1007 CCAGGGTGCAAATATCT 1023

RESULT 7	
AAT70836	
ID AAT70836	standard; cDNA; 2540 BP.
XX	
XX	
AC	AAT70836;
AC	
XX	
DT	02-SEP-1997 (first entry)
XX	
DE	Human apoptosis inhibitor xiap cDNA.
XX	
XX	
KW	Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;
KW	XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;
KW	ischemia; myocardial infarction; stroke;
KW	repertusion injury; toxin-induced liver disease; gene therapy;
KW	diagnosis; ds.
KW	

Qy	61	CGAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTCAAGTGTCTTCCACTGTGGA	120
Db	886	GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGTCTTTCACCTGTGGA	945
Qy	121	GGAGGGGTCAAGGATTGGAGCCCAAGAGACCCCTGGGACACAGCTGCTAAAGTGCTAC	180
Db	946	GGAGGGTCAACTGATTGGAGCCCAAGTGAAGACCCCTGGGAACAACATGCTAAATGGTAT	1005
Qy	181	CCAGGGTGCAAAATACCT	197
Db	1006	CCAGGGTGCAAAATATCT	1022

RESULT 8	
AAA64901	
ID	AAA64901 standard; DNA; 2540 Bp.
XX	
XX	
AC	AAA64901;
AC	
XX	
XX	
DT	07-NOV-2000 (first entry)
DT	
XX	
XX	
DE	Human X-linked inhibitor of apoptosis DNA.
DE	
XX	
XX	
KW	X-linked inhibitor of apoptosis; XIAP; hIAP; U45880;
KW	antisense; antiinflammatory; cytostatic; tumour; ds.
XX	
OS	Homo sapiens.



CC development, viral pathogenesis, autoimmune disorders, neurodegenerative  
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes  
CC virus, pox virus and adenovirus). The present sequence is a human IAP  
CC cDNA sequence.  
XX  
SQ Sequence 2540 BP; 782 A; 415 C; 549 G; 772 T; 22 other;  
Query Match 87.4%; Score 173; DB 24; Length 2540;  
Best Local Similarity 92.4%; Pred. No. 7.5e-50;  
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
Oy 1 TATGAAGCAGGATGCTTACTTTTGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60  
|||||  
Db 826 TATGAAGCAGGATGCTTACTTTTGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 885  
Oy 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA 120  
|||||  
Db 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA 945  
Oy 121 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGCCCTGGGACCAACATGCTAAATGGTAT 180  
|||||  
Db 946 GAGGGCTTAAGTGAAGCCCAAGTGAAGCCCTGGGACCAACATGCTAAATGGTAT 1005  
Oy 181 CCAGGGTGCAAAATACCT 197  
|||||  
Db 1006 CCAGGGTGCAAAATATCT 1022  
RESULT 9  
ID ABK93869 standard; cDNA: 2540 BP.  
XX  
AC ABK93869;  
XX  
DT 26-AUG-2002 (first entry)  
XX  
DE Human cDNA encoding inhibitor of apoptosis, XIAP #1.  
XX  
KW Human; ss: gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;  
KW cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;  
KW pancreatic cancer; embryonic development; viral pathogenesis;  
KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;  
KW lupus erythematosus; herpes virus infection; pox virus infection;  
KW adenovirus infection; proliferative disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200226968-A2.  
XX  
PD 04-APR-2002.  
XX  
PF 27-SEP-2001; 2001WO-CA01379.  
XX  
PR 28-SEP-2000; 2000US-0672717.  
XX  
PA (UYOT-) UNIV OTTAWA.  
PA (AEGE-) AEGERA THERAPEUTICS INC.  
XX  
PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;  
XX  
DR WPI; 2002-479562/51.  
XX  
P-PSDB; ABG65663.  
XX  
PT Novel antisense inhibitor of apoptosis nucleic acid useful for  
PT enhancing apoptosis in a cell, for treating cancer and other  
PT proliferative diseases  
XX  
PS Disclosure; Fig 1; 135pp; English.  
XX  
CC The invention relates to an inhibitor of apoptosis (IAP) antisense  
CC nucleic acid (I) that inhibits IAP biological activity, regardless of  
CC length of the antisense nucleic acid, the IAP proteins may be mouse  
CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical  
CC composition comprising a mammalian IAP antisense molecule and a method of  
CC enhancing apoptosis in a cell, comprising administering a negative  
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP  
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a  
CC mammal diagnosed with a proliferative disease. The method is useful for  
CC treating a patient diagnosed with a proliferative disease like cancer.  
CC The IAP antisense molecule is useful to treat, ameliorate, improve,  
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,  
CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or  
CC conditions where apoptosis is involved or implicated (e.g. embryonic

CC development, viral pathogenesis, autoimmune disorders, neurodegenerative  
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes  
CC virus, pox virus and adenovirus). The present sequence is a human IAP  
CC cDNA sequence.  
XX  
SQ Sequence 2540 BP; 782 A; 415 C; 549 G; 772 T; 22 other;  
Query Match 87.4%; Score 173; DB 24; Length 2540;  
Best Local Similarity 92.4%; Pred. No. 7.5e-50;  
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
Oy 1 TATGAAGCAGGATGCTTACTTTTGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60  
|||||  
Db 826 TATGAAGCAGGATGCTTACTTTTGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 885  
Oy 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA 120  
|||||  
Db 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA 945  
Oy 121 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGCCCTGGGACCAACATGCTAAATGGTAT 180  
|||||  
Db 946 GAGGGCTTAAGTGAAGCCCAAGTGAAGCCCTGGGACCAACATGCTAAATGGTAT 1005  
Oy 181 CCAGGGTGCAAAATACCT 197  
|||||  
Db 1006 CCAGGGTGCAAAATATCT 1022  
RESULT 10  
ID ABK93875 standard; cDNA: 3000 BP.  
XX  
AC ABK93875;  
XX  
DT 26-AUG-2002 (first entry)  
XX  
DE Human cDNA encoding inhibitor of apoptosis, XIAP #2.  
XX  
KW Human; ss: gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;  
KW cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;  
KW pancreatic cancer; embryonic development; viral pathogenesis;  
KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;  
KW lupus erythematosus; herpes virus infection; pox virus infection;  
KW adenovirus infection; proliferative disease.  
XX  
OS Homo sapiens.  
XX  
PN WO200226968-A2.  
XX  
PD 04-APR-2002.  
XX  
PF 27-SEP-2001; 2001WO-CA01379.  
XX  
PR 28-SEP-2000; 2000US-0672717.  
XX  
PA (UYOT-) UNIV OTTAWA.  
PA (AEGE-) AEGERA THERAPEUTICS INC.  
XX  
PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;  
XX  
DR WPI; 2002-479562/51.  
XX  
PT Novel antisense inhibitor of apoptosis nucleic acid useful for  
PT enhancing apoptosis in a cell, for treating cancer and other  
PT proliferative diseases  
XX  
PS Example 2; Fig 15; 135pp; English.  
XX  
CC The invention relates to an inhibitor of apoptosis (IAP) antisense  
CC nucleic acid (I) that inhibits IAP biological activity, regardless of  
CC length of the antisense nucleic acid, the IAP proteins may be mouse  
CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical  
CC composition comprising a mammalian IAP antisense molecule and a method of

enhancing apoptosis in a cell, comprising administering a negative regulator of the IAP anti-apoptotic pathway to the cell. The IAP antisense inhibitor is useful for enhancing apoptosis in a cell in a mammal diagnosed with a proliferative disease. The method is useful for treating a patient diagnosed with a proliferative disease like cancer. The IAP antisense molecule is useful to treat, ameliorate, improve, sustain or prevent proliferative diseases (e.g. ovarian cancer, adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or conditions where apoptosis is involved or implicated (e.g. embryonic development, viral pathogenesis, autoimmune disorders, neurodegenerative diseases, multiple sclerosis, lupus erythematosus and infection by herpes virus, pox virus and adenovirus). The present sequence is a human IAP cDNA sequence.

Sequence 3000 BP; 974 A; 452 C; 601 G; 973 T; 0 other;

Query Match 87.4%; Score 173; DB 24; Length 3000;  
Best Local Similarity 92.4%; Pred. No. 8e-50;  
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

1 TATGAAGCAGCGATCTTACTTTGGACATGGATATCTACGTACACAGGACGCTT 60  
|||||

1482 TATGAAGCAGCGATCTTACTTTGGACATGGATATCTACGTACACAGGACGCTT 1541  
|||||

61 GCAAGAGCTGATTTATGCTTTAGGTGAAGGGGATAAAGTGAAGTCTCCACTGTGGA 120  
|||||

1542 GCAAGAGCTGATTTATGCTTTAGGTGAAGGGGATAAAGTGAAGTCTCCACTGTGGA 1601  
|||||

121 GGAGGGCTCAGGATTTGGAAGCCCAAGTGAAGACCCCTGGGACCAAGTCTAAGTGTGCTAC 180  
|||||

1602 GGAGGGCTAAGTGTGGAAGCCCAAGTGAAGACCCCTGGGACCAAGTCTAAGTGTGCTAT 1661  
|||||

181 CCAGGGTGCAAAATACCT 197  
|||||

1662 CCAGGGTGCAAAATATCT 1678  
|||||

## RESULT 11

AAV55038  
ID AAV55038 standard; cDNA; 5232 BP.

AAV55038;

13-NOV-1998 (first entry)

Human XIAP coding sequence.

Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide; proliferative disease; IAP; therapy; cancer; human; XIAP protein; ss.

Homo sapiens.

Key Location/Qualifiers

CDs 34..1527

/\*tag= a

/product= XIAP

WO9835693-A2.

20-AUG-1998.

13-FEB-1998; 98WO-IB00781.

13-FEB-1997; 97US-0800929.

(UYOT-) UNIV OTTAWA.

Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;

Teang B;

WPI; 1998-467164/40.

P-PSDB; AAW69294.

Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP or NAIP polypeptide - also methods for prognosis based on presence of IAP and NAIP, specifically applied to cancers involving p53 mutations

Claim 13: Fig 1; 147pp; English.

This sequence encodes the human XIAP protein, which is an inhibitor of apoptosis protein (IAP), and can be used in the method of the invention. The method is for enhancing apoptosis in cells from a mammal with proliferative disease by treatment with a compound that inhibits biological activity of an IAP or NAIP polypeptide. The inhibitory compounds are used to treat proliferative diseases, specifically cancers of ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney, liver nasopharynx, thyroid, central nervous system, prostate, colon, rectum, cervix or endometrium, particularly to increase their sensitivity to chemotherapeutic agents. High levels of the IAP or NAIP proteins are detected in many cancers and are associated with poor prognosis, resistance to chemotherapeutic agents and mutations in p53 (it is suggested that wild-type p53 suppresses transcription of the IAP or NAIP genes). Transgenic animals are used for testing the effects of antisense oligonucleotides and for screening for the inhibitors.

Sequence 5232 BP; 1579 A; 861 C; 1062 G; 1728 T; 2 other;

Query Match 87.4%; Score 173; DB 19; Length 5232;

Best Local Similarity 92.4%; Pred. No. 1e-49; Indels 0; Gaps 0;  
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

1 TATGAAGCAGCGATCTTACTTTGGACATGGATATCTACGTACACAGGACGCTT 60  
|||||

826 TATGAAGCAGCGATCTTACTTTGGACATGGATATCTACGTACACAGGACGCTT 885  
|||||

61 GCAAGAGCTGATTTATGCTTTAGGTGAAGGGGATAAAGTGAAGTCTCCACTGTGGA 120  
|||||

886 GCAAGAGCTGATTTATGCTTTAGGTGAAGGGGATAAAGTGAAGTCTCCACTGTGGA 945  
|||||

121 GGAGGGCTCAGGATTTGGAAGCCCAAGTGAAGACCCCTGGGACCAAGTCTAAGTGTGCTAC 180  
|||||

946 GGAGGGCTAAGTGTGGAAGCCCAAGTGAAGACCCCTGGGACCAAGTCTAAGTGTGCTAT 1005  
|||||

181 CCAGGGTGCAAAATACCT 197  
|||||

1006 CCAGGGTGCAAAATATCT 1022  
|||||

## RESULT 12

AA03575

ID AA03575 standard; cDNA; 1752 BP.

AA03575;

19-JUN-2001 (first entry)

Human IAP-like protein-3 (ILP-3) cDNA.

Human; inhibitor of apoptosis; IAP-like protein-3; ILP-3; chromosome 2q12-q14; transforming growth factor beta receptor; TGFbetaR; c-Jun N-terminal kinase; JNK; gene therapy; osteoarthritis; cytostatic; hypothyroidism; juvenile nephronophthisis; thrombophilia; cancer; colorectal cancer; neonatal purpura fulminans; autoimmune disease; diabetes; multiple sclerosis; neurodegenerative disease; retinal degeneration; ss.

Homo sapiens.

Key Location/Qualifiers

CDs 847..1197

/\*tag= a

/product= "Human inhibitor of apoptosis (IAP)-like

protein-3 (hILP-3)"

WO200123568-A2.

XX 05-APR-2001.  
XX 29-SEP-2000; 2000WO-US26735.  
XX 30-SEP-1999; 99US-0157169.  
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX Duckett C, Mir SS;  
XX WPI; 2001-258135/26.  
XX P-PSDB; NAE00359.  
XX Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with  
XX transforming growth factor beta receptor modulating activity, and the  
XX nucleic acids that encode them, useful for treating, e.g. diabetes and  
XX multiple sclerosis .  
XX Claim 18; Page 87-88; 108pp; English.  
XX The present sequence is human inhibitor of apoptosis (IAP)-like protein-3  
XX (ILP-3) cDNA. The ILP-3 gene is located on chromosome 2q12-q14.  
XX ILP-3 comprises a spacer region and a ring finger domain. The ILP  
XX interacts with transforming growth factor beta receptor (TGFbetaR) and  
XX modulates TGFbetaR activity. ILP-3 also moderately inhibits ILP-1.  
XX mediated c-Jun N-terminal kinase (JNK) activation when co-transfected  
XX with ILP-1. Such activity decreases or prevents apoptosis in a cell.  
XX ILP-3 is used in the area of genetic testing for predisposition to  
XX diseases, such as osteoarthritis, hypothyroidism, juvenile  
XX nephronophthisis, thrombophilia, colorectal cancer and neonatal purpura  
XX fulminans owing to an ILP-3 deletion or mutation. The ILP is also used  
XX in the treatment of diseases associated with abnormal apoptosis such as  
XX cancer, autoimmune diseases, e.g., diabetes and multiple sclerosis and  
XX neurodegenerative diseases including retinal degeneration. The ILP-3  
XX gene is also used in gene therapy for treating patients suffering from  
XX ILP-3 gene deletions or mutations.  
XX Sequence 1752 BP; 530 A; 299 C; 385 G; 538 T; 0 other;

Query Match 79.3%; Score 157; DB 22; Length 1752;  
Best Local Similarity 87.3%; Pred. No. 2.4e-44;  
Matches 172; Conservative 0; Mismatches 25; Indels 0; Gaps 0;  
QY 1 TATGAAGCAGCGATGTTTCTTCTTGGACATGATATCTACTAGTTAAACAAGGAGCAGCTT 60  
DB 499 TATGAAGCAGCGATGATTTCTTCTTGGATGCGATATATCTACTAGTTAAACAAGGAGCAGCTT 558  
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120  
DB 559 TCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 618  
QY 121 GGAGGGCTCAGGATGGAAGCCAGTGAAGACCCCTGGGACCGACGATGCTTAAGTCTGCTAC 180  
DB 619 GGGGGGCTAACTGATTTGAAGCCGACGAGACCCCTGGGACCAACATGATAAATGGCAT 678  
QY 181 CCAGGGTGAATACCT 197  
DB 679 CCAGGGTGAATATCT 695

RESULT 13  
ABK14677  
ID ABK14677 standard; cDNA; 1758 BP.  
XX  
AC ABK14677;  
XX 08-MAY-2002 (first entry)  
XX Human Inhibitor of apoptosis protein 7 (IAPL7) cDNA.  
XX  
XX Human; gene; inhibitor of apoptosis 7; IAPL7; cytostatic;  
KW antiapoptotic; IAP; apoptosis; antibody; V-Rel; NF-kappaB;

KW chromosome 19; vaccine; gene therapy; hyperproliferative disease;  
KW cancer; transgenic animal; ss.  
XX Homo sapiens.  
XX Location/Qualifiers  
XX Key 286..1680  
XX CDS /\*tag= a  
XX /product= "IAPL7 protein"  
XX /partial  
XX /note= "No start codon shown"  
XX WO200210381-A1.  
XX 07-FEB-2002.  
XX 18-JUL-2001; 2001WO-EP08287.  
XX 28-JUL-2000; 2000EP-0116452.  
XX (MERE ) MERCK PATENT GMBH.  
XX Hentsch B;  
XX WPI; 2002-188741/24.  
XX P-PSDB; NAE075747.  
XX New inhibitor of apoptosis proteins and polynucleotides useful in  
XX vaccines for inducing an immune response against hyperproliferative  
XX diseases e.g. cancer  
XX Claim 5; Page 33-35; 41pp; English.  
XX This invention relates to the nucleic acid and protein sequences of a  
XX novel inhibitor apoptosis protein (IAPL7) polypeptide. These sequences  
XX have homology to the IAP (inhibitors of apoptosis) gene family which  
XX are thought to inhibit proteins by regulating the anti-apoptotic  
XX activity of the V-Rel and NF-kappaB family of transcription factors.  
XX The gene for IAPL7 is located on human chromosome 19. The nucleic acids  
XX of the invention are useful for screening to identify compounds that  
XX stimulate or inhibit the function or level of IAPL7, where the  
XX identified compounds are useful for treating hyper-proliferative  
XX diseases such as cancer. The protein sequences may also be used to  
XX identify membrane bound or soluble receptors of IAPL7 by standard  
XX receptor binding techniques. Nucleic acids encoding IAPL7, may be used  
XX as hybridisation probes for cDNA and genomic DNA, or as primers for  
XX nucleic acid amplification reaction and the primers and probes may also  
XX be used to isolate full-length cDNAs and genomic clones encoding IAPL7.  
XX The nucleic acid sequences are useful as diagnostic reagents for  
XX diagnosing a disease or a susceptibility to a disease by detecting  
XX mutations in the associated gene. The nucleic acid sequence is useful  
XX for chromosome localisation and tissue expression studies and is also  
XX useful for producing transgenic animals. The IAPL7 protein sequence may  
XX also be used to generate an anti-IAPL7 antibody which is useful in  
XX screening methods for detecting the effect of added compounds on the  
XX production of mRNA and protein in cells. The sequences of the invention  
XX are also useful as vaccines for inducing an immunological response in a  
XX mammal. The present sequence represents the cDNA encoding the human  
XX inhibitor of apoptosis 7 (IAP7) protein of the invention.  
XX Sequence 1758 BP; 488 A; 371 C; 470 G; 429 T; 0 other;

Query Match 75.3%; Score 149; DB 24; Length 1758;  
Best Local Similarity 84.8%; Pred. No. 1.5e-41;  
Matches 167; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
QY 1 TATGAAGCAGCGATGTTTCTTCTTGGACATGATATCTACTAGTTAAACAAGGAGCAGCTT 60  
DB 979 TATGAAGCAGCGCTCATTTCTTCTTGGACATGATATCTACTAGTTAAACAAGGAGCAGCTT 1038  
QY 61 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 120  
DB 1039 GCAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGTGAAGTCTTCCACTGTGGA 1098

This invention relates to the nucleic acid and protein sequences of a novel inhibitor apoptosis protein (IAP17) polypeptide. These sequences have homology to the IAP (inhibitors of apoptosis) gene family which are thought to inhibit proteins by regulating the anti-apoptotic activity of the v-Rel and NF-kappaB family of transcription factors. The gene for IAP17 is located on human chromosome 19. The nucleic acids of the invention are useful for screening to identify compounds that stimulate or inhibit the function or level of IAP17, where the identified compounds are useful for treating hyper-proliferative diseases such as cancer. The protein sequences may also be used to identify membrane bound or soluble receptors of IAP17 by standard receptor binding techniques. Nucleic acids encoding IAP17, may be used as hybridisation probes for cDNA and genomic DNA, or as primers for nucleic acid amplification reaction and the primers and probes may also be used to isolate full-length cDNAs and genomic clones encoding IAP17. The nucleic acid sequences are useful as diagnostic reagents for diagnosing a disease or a susceptibility to a disease by detecting

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Duckett C, Mir SS;  
XX  
XX WPI; 2001-258135/26.  
XX DR

DR P-PSDB; AAE00365.

PT Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with

PT transforming growth factor beta receptor modulating activity, and the

PT nucleic acids that encode them, useful for treating, e.g. diabetes and

PT multiple sclerosis -

XX

PS Claim 18; Page 94-98; 108pp; English.

XX

CC The present sequence is human inhibitor of apoptosis (IAP)-like protein-2

CC (ILP-2), cDNA. The hILP-2 gene is located on chromosome 19q13.3-q13.4

CC ILP-2 comprises a single amino-terminal domain known as baculovirus iap

CC repeat (BIR), followed by a spacer region and a carboxy-terminal iap

CC finger domain. It interacts with transforming growth factor beta

CC receptor (TGFbetaR) and modulates TGFbetaR activity. It also potentially

CC inhibits apoptosis induced by overexpression of Bax or by Caspase-9 and

CC Apaf-1. It also activates c-Jun N-terminal kinase (JNK) activity. ILP-2

CC is used in the area of genetic testing for predisposition to diseases,

CC such as cone-rod retinal dystrophy-2, retinitis pigmentosa,

CC glutaricaciduria, T-cell acute lymphoblastic leukaemia, colorectal cancer

CC and hyperferritinemia-cataract syndrome owing to an ILP-2 deletion or

CC mutation. The ILP is also used in the treatment of diseases associated

CC with abnormal apoptosis such as cancer, autoimmune diseases, e.g.,

CC diabetes and multiple sclerosis and neurodegenerative diseases including

CC retinal degeneration. The ILP-2 gene is also used in gene therapy for

CC treating patients suffering from ILP-2 gene deletions or mutations.

XX

XX Sequence 4993 BP; 1526 A; 973 C; 1196 G; 1297 T; 1 other;

XX

Query Match 75.3%; Score 149; DB 22; Length 4993;

Best Local Similarity 84.8%; Pred. No. 2.3e-41;

Matches 167; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGAACTGGATATCTCAGTTAACAGGAGCAGCTT 60

DB 2083 TATGAAGCCGCGCTCATTTACTTTTGGGACATGGATGTACTCCGTTAACAAAGAGCAGCTT 2142

QY 61 GCAAGAGCTGGATTTTATGCTTTTAGTGTGAGGCGATAAGTGAAGTGTCTTCACGTGTGGA 120

DB 2143 GCAAGAGCTGGATTTTATGCTTCTAGTCTCAGAGAGATAAGTACAGTGTCTTCACGTGTGGA 2202

QY 121 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGGACACGATGCTAAAGTGCTAC 180

DB 2203 GGAGGGCTTAGCCAACTGGAGCCCAAGGAAGATCCTTGGGAACAGCATGCTAAATGGTAT 2262

QY 181 CCAGGGTGCAAATACCT 197

DB 2263 CCAGGTTGCAATATCT 2279

Search completed: April 19, 2003, 01:52:57  
Job time : 157 secs

GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2003, 01:53:06 ; Search time 43 Seconds  
(without alignments)  
1412.140 Million cell updates/sec

Title: US-09-654-743-51

Perfect score: 198

Sequence: 1 tatgaagcagcgatgttac.....accacgggtgcaataccta 198

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_NA.\*  
1: /cgn2\_6/ptodata/1/lna/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/lna/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/lna/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/lna/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/lna/PTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/lna/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	198	100.0	2100	2	US-08-511-485-9		Sequence 9, Appli
2	194.8	98.4	2691	3	US-09-212-971-9		Sequence 9, Appli
3	194.8	98.4	2691	3	US-08-800-929A-9		Sequence 9, Appli
4	194.8	98.4	2691	4	US-09-617-053A-9		Sequence 9, Appli
5	173	87.4	1588	4	US-09-239-867-3		Sequence 3, Appli
6	173	87.4	2540	2	US-08-511-485-3		Sequence 3, Appli
7	173	87.4	2540	2	US-09-332-580-1		Sequence 3, Appli
8	173	87.4	5232	3	US-09-212-971-3		Sequence 1, Appli
9	173	87.4	5232	3	US-08-800-929A-3		Sequence 3, Appli
10	173	87.4	5232	3	US-09-617-053A-3		Sequence 3, Appli
11	147.4	74.4	711	3	US-09-121-979-3		Sequence 3, Appli
12	147.4	74.4	711	3	US-09-332-319-3		Sequence 3, Appli
13	147.4	74.4	1559	4	US-09-239-867-1		Sequence 3, Appli
14	134.4	67.9	15231	3	US-09-128-155-16		Sequence 16, Appl
15	109.6	55.4	176373	4	US-09-128-155-17		Sequence 17, Appl
16	76	38.4	2601	4	US-08-569-749-3		Sequence 3, Appli
17	76	38.4	2601	5	PCT-US96-12860-3		Sequence 3, Appli
18	76	38.4	2676	2	US-08-511-485-5		Sequence 5, Appli
19	76	38.4	3076	2	US-09-205-144-1		Sequence 5, Appli
20	76	38.4	6669	3	US-09-212-971-5		Sequence 1, Appli
21	76	38.4	6669	3	US-08-800-929A-5		Sequence 5, Appli
22	76	38.4	6669	4	US-09-617-053A-5		Sequence 5, Appli
23	68	34.3	2676	3	US-09-212-971-11		Sequence 11, Appl
24	68	34.3	2676	3	US-08-800-929A-11		Sequence 11, Appl
25	68	34.3	2676	4	US-09-617-053A-11		Sequence 11, Appl
26	65.8	33.2	1435	5	PCT-US95-05922A-1		Sequence 1, Appli
27	65.8	33.2	2580	2	US-08-511-485-7		Sequence 7, Appli

## ALIGNMENTS

## RESULT 1

US-08-511-485-9

; Sequence 9, Application US/08511485

; Patent No. 5919912

; GENERAL INFORMATION:

; APPLICANT: Korneluk, Robert G.

; APPLICANT: Mackenzie, Alexander E.

; APPLICANT: Baird, Stephen

; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,

; TITLE OF INVENTION: PROBES, AND DETECTION METHODS

; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fish & Richardson P.C.

; STREET: 225 Franklin Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110-2804

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/511,485

; FILING DATE: 04-AUG-1995

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Clark, Paul T.

; REGISTRATION NUMBER: 30,162

; REFERENCE/DOCKET NUMBER: 07540/002001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617/542-5070

; TELEX: 617/542-8906

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2100 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: both

; MOLECULE TYPE: DNA (genomic)

US-08-511-485-9

Query Match

Best Local Similarity 100.0%; Score 198; DB 2; Length 2100;

Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy

1 TATGAAGCAGCGATGTCTTTGGACATGGATATACGTAAACAGGACGCTT 60  
|||||

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Sequence 7, Appli  
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Sequence 13, Appli  
Sequence 13, Appli  
Sequence 13, Appli  
Sequence 13, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 10, Appli  
Sequence 2, Appli  
Sequence 1, Appli  
Sequence 1, Appli

Db 916 TATGAAGCAGCGATCGTTACTTTTGAACATGGATATACCTAGTTAAACAGGACGACGTT 975  
QY 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGCCGATTAAGTGAAGTCTCCACTGTGGA 120  
Db 976 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGCCGATTAAGTGAAGTCTCCACTGTGGA 1035  
QY 121 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGTCTAC 180  
Db 1036 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGTCTAC 1095  
QY 181 CCAGGGTGCAAAATACCTA 198  
Db 1096 CCAGGGTGCAAAATACCTA 1113

## RESULT 2

US-09-212-971-9  
; Sequence 9, Application US/09212971B  
; Patent No. 6107041  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: Mackenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; FILE REFERENCE: 07891/009002  
; CURRENT APPLICATION NUMBER: US/09/212,971B  
; EARLIER FILING DATE: 1998-12-16  
; EARLIER APPLICATION NUMBER: 60/017,354  
; EARLIER FILING DATE: 1996-04-26  
; EARLIER APPLICATION NUMBER: 60/030,590  
; EARLIER FILING DATE: 1996-11-14  
; EARLIER APPLICATION NUMBER: 08/800,929  
; EARLIER FILING DATE: 1997-02-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 2691  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-212-971-9

Query Match 98.4%; Score 194.8; DB 3; Length 2691;  
Best Local Similarity 99.0%; Pred. No. 1.9e-60;  
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGAACATGGATATACCTAGTTAAACAGGACGACGTT 1520  
Db 1461 TATGAAGCAGCGATCGTTACTTTTGAACATGGATATACCTAGTTAAACAGGACGACGTT 1520  
QY 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGCCGATTAAGTGAAGTCTCCACTGTGGA 120  
Db 1521 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGCCGATTAAGTGAAGTCTCCACTGTGGA 1580  
QY 121 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGTCTAC 180  
Db 1581 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGTCTAC 1640  
QY 181 CCAGGGTGCAAAATACCTA 198  
Db 1641 CCAGGGTGCAAAATACCTA 1658

## RESULT 3

US-08-800-929A-9  
; Sequence 9, Application US/08800929A  
; Patent No. 613437  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G

; APPLICANT: MacKenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF  
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Clark & Elbing LLP  
; STREET: 176 Federal Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02110  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/800,929A  
; FILING DATE: 13-FEB-1997  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/030,590  
; FILING DATE: 14-NOV-1996  
; APPLICATION NUMBER: 60/017,354  
; FILING DATE: 26-APR-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bieker-Brady, Kristina  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 07891/009001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-428-0200  
; TELEFAX: 617-428-7045  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2691 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-800-929A-9

Query Match 98.4%; Score 194.8; DB 3; Length 2691;  
Best Local Similarity 99.0%; Pred. No. 1.9e-60;  
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGAACATGGATATACCTAGTTAAACAGGACGACGTT 60  
Db 1461 TATGAAGCAGCGATCGTTACTTTTGAACATGGATATACCTAGTTAAACAGGACGACGTT 1520  
QY 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGCCGATTAAGTGAAGTCTCCACTGTGGA 120  
Db 1521 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGCCGATTAAGTGAAGTCTCCACTGTGGA 1580  
QY 121 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGTCTAC 180  
Db 1581 GGAGGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGGACCAAGCATGCTAAGTGTCTAC 1640  
QY 181 CCAGGGTGCAAAATACCTA 198  
Db 1641 CCAGGGTGCAAAATACCTA 1658

## RESULT 4

US-09-617-053A-9  
; Sequence 9, Application US/09617053A  
; Patent No. 6300492  
; GENERAL INFORMATION:

```

; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-617-053A-9

Query Match      98.4%; Score 194.8; DB 4; Length 2691;
Best Local Similarity 99.0%; Pred. No. 1.9e-60;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 60
DB 1461 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 1520

QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGATAAGTGAAGTGTCTCCACTGTGGA 120
DB 1521 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGATAAGTGAAGTGTCTCCACTGTGGA 1580

QY 121 GGAGGCTCAGCGATTTGAAGCCAGTGAAGACCCCTGGGACCAGCATGCTTAAGTGTAC 180
DB 1581 GGAGGCTCAGCGATTTGAAGCCAGTGAAGACCCCTGGGACCAGCATGCTTAAGTGTAC 1640

QY 181 CCAGGTCGAATACCTA 198
DB 1641 CCAGGTCGAATACCTA 1658

RESULT 5
US-09-239-867-3
; Sequence 3, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT FILING DATE: 1999-01-29
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-239-867-3

Query Match      87.4%; Score 173; DB 4; Length 1588;
Best Local Similarity 92.4%; Pred. No. 1.1e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 60
DB 826 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGATAAGTGAAGTGTCTCCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGATAAGTGAAGTGTCTCCACTGTGGA 945

QY 121 GGAGGCTCAGCGATTTGAAGCCAGTGAAGACCCCTGGGACCAGCATGCTTAAGTGTAC 180
DB 946 GGAGGCTCAGCGATTTGAAGCCAGTGAAGACCCCTGGGACCAGCATGCTTAAGTGTAC 1005

QY 181 CCAGGTCGAATACCT 197
DB 1006 CCAGGTCGAATACCT 1022

RESULT 6
US-08-511-485-3
; Sequence 3, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2540 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
US-08-511-485-3

Query Match      87.4%; Score 173; DB 2; Length 2540;
Best Local Similarity 92.4%; Pred. No. 1.3e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 60
DB 826 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGATAAGTGAAGTGTCTCCACTGTGGA 120
DB 886 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGATAAGTGAAGTGTCTCCACTGTGGA 945

QY 121 GGAGGCTCAGCGATTTGAAGCCAGTGAAGACCCCTGGGACCAGCATGCTTAAGTGTAC 180
DB 946 GGAGGCTCAGCGATTTGAAGCCAGTGAAGACCCCTGGGACCAGCATGCTTAAGTGTAC 1005

QY 181 CCAGGTCGAATACCT 197
DB 1006 CCAGGTCGAATACCT 1022
```



Db 1006 CCAGGGTGCAAAATATCT 1022  
|||||

## RESULT 7

US-09-392-580-1

; Sequence 1, Application US/09392580

; Patent No. 6087173

; GENERAL INFORMATION:

; APPLICANT: C. Frank Bennett

; APPLICANT: Elizabeth J. Ackermann

; APPLICANT: Lex M. Cowser

; TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSION

; FILE REFERENCE: RTS-0072

; CURRENT APPLICATION NUMBER: US/09/392,580

; CURRENT FILING DATE: 1999-09-09

; NUMBER OF SEQ ID NOS: 47

; SEQ ID NO 1

; LENGTH: 2540

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (34)..(1527)

US-09-392-580-1

Query Match 87.4%; Score 173; DB 3; Length 2540;

Best Local Similarity 92.4%; Pred. No. 1.3e-52;

Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATGCTTACTTTTGGACATGGATATATCTCAGTTAAACAGGAGCAGCTT 60

Db 826 TATGAAGCAGCGATGCTTACTTTTGGACATGGATATATCTCAGTTAAACAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGATTAAGTGAAGTGCCTTCCACTGTGGA 120

Db 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGATTAAGTGAAGTGCCTTCCACTGTGGA 945

QY 121 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGGACCATGCTTAAGTGTCTAC 180

Db 946 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGGACCATGCTTAAGTGTCTAC 1005

QY 181 CCAGGGTGCAAAATATCT 197

Db 1006 CCAGGGTGCAAAATATCT 1022

## RESULT 8

US-09-212-971-3

; Sequence 3, Application US/09212971B

; Patent No. 6107041

; GENERAL INFORMATION:

; APPLICANT: Korneluk, Robert G

; APPLICANT: Mackenzie, Alexander E

; APPLICANT: Liston, Peter

; APPLICANT: Baird, Stephen

; APPLICANT: Tsang, Benjamin K

; APPLICANT: Pratt, Christine

; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND

; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE

; TITLE OF INVENTION: DISEASE

; FILE REFERENCE: 07891/009002

; CURRENT APPLICATION NUMBER: US/09/212,971B

; CURRENT FILING DATE: 1998-12-16

; EARLIER APPLICATION NUMBER: 60/017,354

; EARLIER FILING DATE: 1996-04-26

; EARLIER APPLICATION NUMBER: 60/030,590

; EARLIER FILING DATE: 1996-11-14

; EARLIER APPLICATION NUMBER: 08/800,929

; EARLIER FILING DATE: 1997-02-13

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

LENGTH: 5232  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: variation  
LOCATION: (4623)...(4623)  
OTHER INFORMATION: n can be any nucleotide  
FEATURE:  
NAME/KEY: variation  
LOCATION: (4622)...(4622)  
OTHER INFORMATION: n can be any nucleotide  
US-09-212-971-3

Query Match 87.4%; Score 173; DB 3; Length 5232;

Best Local Similarity 92.4%; Pred. No. 1.9e-52;

Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATGCTTACTTTTGGACATGGATATATCTCAGTTAAACAGGAGCAGCTT 60

Db 826 TATGAAGCAGCGATGCTTACTTTTGGACATGGATATATCTCAGTTAAACAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGATTAAGTGAAGTGCCTTCCACTGTGGA 120

Db 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCGATTAAGTGAAGTGCCTTCCACTGTGGA 945

QY 121 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGGACCATGCTTAAGTGTCTAC 180

Db 946 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGGACCATGCTTAAGTGTCTAC 1005

QY 181 CCAGGGTGCAAAATATCT 197

Db 1006 CCAGGGTGCAAAATATCT 1022

## RESULT 9

US-08-800-929A-3

; Sequence 3, Application US/08800929A

; Patent No. 6133437

; GENERAL INFORMATION:

; APPLICANT: Korneluk, Robert G

; APPLICANT: Mackenzie, Alexander E

; APPLICANT: Liston, Peter

; APPLICANT: Baird, Stephen

; APPLICANT: Tsang, Benjamin K

; APPLICANT: Pratt, Christine

; TITLE OF INVENTION: DETECTION AND MODULATION OF

; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT

; TITLE OF INVENTION: DISEASE

; NUMBER OF SEQUENCES: 17

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Clark &amp; Elbing LLP

; STREET: 176 Federal Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02110

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/800,929A

; FILING DATE: 13-FEB-1997

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/030,590

; FILING DATE: 14-NOV-1996

; APPLICATION NUMBER: 60/017,354

; FILING DATE: 26-APR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Bleker-Brady, Kristina

; REGISTRATION NUMBER:

```
/ REFERENCE/DOCKET NUMBER: 07891/009001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-428-0200
/ TELEFAX: 617-428-7045
/
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5232 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: Other
/ LOCATION: 1..5232
/ OTHER INFORMATION: N at 4622 and 4633 can be A, G, T or C.
US-08-800-929A-3

Query Match      87.4%; Score 173; DB 3; Length 5232;
Best Local Similarity 92.4%; Pred. No. 1.9e-52;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGAACTGATATCTAGTTAAACAAGGAGCAGCTT 60
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Db 826 TATGAAGCAGCGATCGTTACTTTTGGACATGATATCTAGTTAAACAAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAGTGAAGTGTTCACCTGTGGA 120
   |||||
Db 886 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAGTGAAGTGTTCACCTGTGGA 120

QY 121 GGAGGGCTCAGCGATTGGAAGCAAGTGAAGACCCCTGGGACCAACAGTCTAAGTGCTAC 180
   |||||
Db 946 GGAGGGCTCAGCGATTGGAAGCAAGTGAAGACCCCTGGGACCAACAGTCTAAGTGCTAC 180

QY 181 CCAGGGTGCAAAATACCT 197
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Db 1006 CCAGGGTGCAAAATATCT 1022

RESULT 11
US-09-121-979-3
; Sequence 3, Application US/09121979
; Patent No. 6159709
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
; FILE REFERENCE: 07891/021001
; CURRENT APPLICATION NUMBER: US/09/121.979
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-121-979-3

Query Match      74.4%; Score 147.4; DB 3; Length 711;
Best Local Similarity 84.3%; Pred. No. 1.2e-43;
Matches 166; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCGTTACTTTTGGAACTGATATCTAGTTAAACAAGGAGCAGCTT 60
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Db 10 TATGAAGCAGCGATCGTTACTTTTGGACATGATATCTAGTTAAACAAGGAGCAGCTT 69

QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAGTGAAGTGTTCACCTGTGGA 120
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Db 70 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAGTGAAGTGTTCACCTGTGGA 129

QY 121 GGAGGGCTCAGCGATTGGAAGCAAGTGAAGACCCCTGGGACCAACAGTCTAAGTGCTAC 180
   |||||
Db 130 GGAGGGCTCAGCGATTGGAAGCAAGTGAAGACCCCTGGGACCAACAGTCTAAGTGCTAC 180

QY 181 CCAGGGTGCAAAATACCT 197
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Db 190 CCAGGGTGCAAAATATCT 206

RESULT 12
US-09-332-319-3
; Sequence 3, Application US/09332319
; Patent No. 6171821
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
; FILE REFERENCE: 07891/021002
; CURRENT APPLICATION NUMBER: US/09/332.319
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; CURRENT FILING DATE: 1999-06-14  
; EARLIER APPLICATION NUMBER: 09/121,979  
; EARLIER FILING DATE: 1998-07-24  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 711  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-332-319-3

Query Match 1 74.4%; Score 147.4; DB 4; Length 711;  
Best Local Similarity 84.3%; Pred. No. 1.2e-43;  
Matches 166; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
QY 1 TATGAAGCAGCGATCTTACTTTTGAACATGGATATACCTAGTTAACAGGAGCAGCTT 60  
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QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA 120  
DB 70 GCAAGAGCTGGATTTATGCTTATAGTCAAGAGGATAAAGTACAGTGTCTTCCACTGTGGA 129  
QY 121 GGAGGCTCAGCGATTTGGAAGCAAGTGAAGCCCTGGACCATGCTTAAGTGCTAC 180  
DB 130 GGAGGCTAGCCCAAGTGAAGCCCAAGGAGATCTTGGAAACAGCATGCTAAATGGTAT 189  
QY 181 CCAGGTGCAAAATACCT 197  
DB 190 CCAGGTGCAAAATATCT 206

RESULT 13  
US-09-239-867-1  
; Sequence 1, Application US/09239867  
; Patent No. 6331412  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Korneluk et al.  
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING  
; FILE OF INVENTION: MALE FERTILITY  
; FILE REFERENCE: 07891/018002  
; CURRENT APPLICATION NUMBER: US/09/239,867  
; CURRENT FILING DATE: 1999-01-29  
; PRIOR APPLICATION NUMBER: 60/073,001  
; PRIOR FILING DATE: 1998-01-29  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1559  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc.feature  
; LOCATION: (1)...(1559)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-239-867-1

Query Match 74.4%; Score 147.4; DB 4; Length 1559;  
Best Local Similarity 84.3%; Pred. No. 1.8e-43;  
Matches 166; Conservative 0; Mismatches 31; Indels 0; Gaps 0;  
QY 1 TATGAAGCAGCGATCTTACTTTTGAACATGGATATACCTAGTTAACAGGAGCAGCTT 60  
DB 800 TATGAAGCAGCGATCTTACTTTTGGACATGGATGCTCCGTCAACAAGAGCAGCTT 859  
QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA 120  
DB 860 GCAAGAGCTGGATTTATGCTTATAGTCAAGAGGATAAAGTACAGTGTCTTCCACTGTGGA 919  
QY 121 GGAGGCTCAGCGATTTGGAAGCAAGTGAAGCCCTGGACCATGCTTAAGTGCTAC 180  
DB 920 GGAGGCTAGCCCAAGTGAAGCCCAAGGAGATCTTGGAAACAGCATGCTAAATGGTAT 979

QY 181 CCAGGTGCAAAATACCT 197  
DB 980 CCAGGTGCAAAATATCT 996  
RESULT 14  
US-09-128-155-16/c  
; Sequence 16, Application US/09128155  
; Patent No. 6117654  
; GENERAL INFORMATION:  
; APPLICANT: Pan, Yang  
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
; FILE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: 09404/052001  
; CURRENT APPLICATION NUMBER: US/09/128,155  
; CURRENT FILING DATE: 1998-08-03  
; EARLIER APPLICATION NUMBER: US 60/091,650  
; EARLIER FILING DATE: 1998-07-02  
; EARLIER APPLICATION NUMBER: US 60/054,646  
; EARLIER FILING DATE: 1997-08-04  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 16  
; LENGTH: 152331  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc.feature  
; LOCATION: (1)...(152331)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-128-155-16

Query Match 67.9%; Score 134.4; DB 3; Length 152331;  
Best Local Similarity 83.2%; Pred. No. 7.1e-38;  
Matches 164; Conservative 0; Mismatches 32; Indels 1; Gaps 1;  
QY 1 TATGAAGCAGCGATCTTACTTTTGAACATGGATATACCTAGTTAACAGGAGCAGCTT 60  
DB 3298 TATGAAGCAGCGATCTTACTTTTGGATGTGATATATTCAGTTAACAGGAGCAGCTT 3239  
QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATAAAGTGAAGTGTCTTCCACTGTGGA 120  
DB 3238 TCAAGAGCTGGATTTATGCTTTAGTGAAGTGTGATTAAGTGTCTTCCACTGTGGA 3179  
QY 121 GGAGGCTCAGCGATTTGGAAGCAAGTGAAGCCCTGGACCATGCTTAAGTGCTAC 180  
DB 3178 GGGGGCTAAGTGTGGAAGCCCAAGCAGGAA-AACCTTGGGACACATATAAATGGAT 3120  
QY 181 CCAGGTGCAAAATACCT 197  
DB 3119 CCAGGTGCAAAATATCT 3103

RESULT 15  
US-09-128-155-17  
; Sequence 17, Application US/09128155  
; Patent No. 6117654  
; GENERAL INFORMATION:  
; APPLICANT: Pan, Yang  
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY  
; FILE OF INVENTION: AND USES THEREOF  
; FILE REFERENCE: 09404/052001  
; CURRENT APPLICATION NUMBER: US/09/128,155  
; CURRENT FILING DATE: 1998-08-03  
; EARLIER APPLICATION NUMBER: US 60/091,650  
; EARLIER FILING DATE: 1998-07-02  
; EARLIER APPLICATION NUMBER: US 60/054,646  
; EARLIER FILING DATE: 1997-08-04  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 176373  
; TYPE: DNA

GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2003, 02:27:21 ; Search time 66 Seconds  
(without alignments)  
3013.686 Million cell updates/sec

Title: US-09-654-743-51

Perfect score: 198

Sequence: 1 tatgaagcagctgcttac.....accaggtgcaataaccta 198

Scoring table: IDENTITY\_NUC

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Total number of hits satisfying chosen parameters: 1279498

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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  - 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
  - 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
  - 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
  - 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
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  - 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
  - 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
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  - 11: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
  - 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	198	100.0	2100	9	US-09-201-936-9
2	194.8	98.4	2691	10	US-09-974-592-9
3	173	87.4	2404	9	US-09-964-899-38
4	173	87.4	2540	9	US-09-201-936-3
5	173	87.4	2532	10	US-09-974-592-3
6	134.4	67.9	152331	9	US-10-095-407-16
7	109.6	55.4	176373	9	US-10-095-407-17
8	76	38.4	2676	9	US-09-201-936-5
9	76	38.4	3076	9	US-09-954-531-16
10	76	38.4	3076	10	US-09-954-456-1635
11	76	38.4	6669	10	US-09-974-592-5
12	68	34.3	2450	9	US-09-201-936-39
13	68	34.3	2676	10	US-09-974-592-11
14	65.8	33.2	2580	9	US-09-201-936-7
15	65.8	33.2	3532	10	US-09-880-107-3354
16	65.8	33.2	3732	10	US-09-974-592-7
17	61	30.8	3151	10	US-09-974-592-13
18	59.4	30.0	2416	9	US-09-201-936-41
19	56.4	28.5	3773	9	US-10-041-859-1

20	45	22.7	5504	8	US-08-913-322-1	Sequence 1, Appli
21	45	22.7	6124	8	US-08-913-322-21	Sequence 21, Appl
22	45	22.7	6124	10	US-09-967-768A-184	Sequence 184, App
23	45	22.7	6133	8	US-08-913-322-2	Sequence 2, Appli
24	45	22.7	6228	8	US-08-913-322-23	Sequence 23, Appl
25	39.8	20.1	2291	10	US-09-778-927A-21	Sequence 21, Appl
26	34.8	17.6	240	9	US-09-786-692-3493	Sequence 3493, Ap
27	33.2	16.8	240	9	US-09-786-692-6687	Sequence 6687, Ap
28	31.2	15.8	2326	9	US-10-011-585A-6	Sequence 6, Appli
29	30.6	15.5	2790	10	US-09-739-254-30	Sequence 30, Appl
30	30.6	15.5	2790	10	US-09-904-615-30	Sequence 30, Appl
31	30.4	15.4	2000	9	US-09-938-842A-3000	Sequence 3000, Ap
32	29.2	14.7	1011	10	US-09-770-445-222	Sequence 222, App
33	28.8	14.5	2265	9	US-09-938-842A-1065	Sequence 1065, Ap
34	28.4	14.3	1503841	9	US-09-946-807-1	Sequence 1, Appli
35	28.4	14.3	1503841	10	US-09-795-668-1	Sequence 1, Appli
36	28.4	14.3	1503841	10	US-09-795-668-1	Sequence 1, Appli
37	27.8	14.0	3411	10	US-09-925-302-189	Sequence 189, App
38	27.8	14.0	19172	10	US-09-764-877-3474	Sequence 3474, Ap
39	27.6	13.9	2160	9	US-10-115-195-1	Sequence 1, Appli
40	27.6	13.9	6911	9	US-10-170-528-1	Sequence 1, Appli
41	27.6	13.9	197997	10	US-09-822-246-3	Sequence 3, Appli
42	27.4	13.8	75899	10	US-09-854-883-243	Sequence 243, App
43	27.2	13.7	698	10	US-09-770-149-274	Sequence 274, App
44	27.2	13.7	766	10	US-09-770-445-933	Sequence 933, App
45	27.2	13.7	5031	10	US-09-764-877-2950	Sequence 2950, Ap

## ALIGNMENTS

RESULT 1  
US-09-201-936-9  
; Sequence 9, Application US/09201936  
; Publication No. US20020187946A1  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: Mackenzie, Alexander E.  
; APPLICANT: Baird, Stephen  
; APPLICANT: Liston, Peter  
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
; FILE OF INVENTION: PROBS, AND DETECTION METHODS  
; FILE REFERENCE: 07891/003003  
; CURRENT APPLICATION NUMBER: US/09/201.936  
; CURRENT FILING DATE: 1998-12-01  
; EARLIER APPLICATION NUMBER: 09/011.356  
; EARLIER FILING DATE: 1998-02-04  
; EARLIER APPLICATION NUMBER: PCT/IB96/01022  
; EARLIER FILING DATE: 1996-08-05  
; EARLIER APPLICATION NUMBER: 08/576.956  
; EARLIER FILING DATE: 1995-12-22  
; EARLIER APPLICATION NUMBER: 08/511.485  
; EARLIER FILING DATE: 1995-08-04  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 2100  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-201-936-9

Query Match	100.0%	Score 198;	DB 9;	Length 2100;
Best Local Similarity	100.0%	Pred. No. 2.5e-59;		
Matches 198;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy 1	TATGAAGCAGCGATCGTTACTTTTGGACATGATATCTAGTTAAACAAGGAGCAGCTT	60		
Db 916	TATGAAGCAGCGATCGTTACTTTTGGACATGATATCTAGTTAAACAAGGAGCAGCTT	975		
Qy 61	GCACAGCTGGATTTTATGCTTTTAGTGAAGCGGATAAGTGAAGTGTTCACGTGGA	120		
Db 976	GCACAGCTGGATTTTATGCTTTTAGTGAAGCGGATAAGTGAAGTGTTCACGTGGA	1035		

QY 121 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGGACCCAGCATGCTAAAGTGCTAC 180  
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Db 1036 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGGACCCAGCATGCTAAAGTGCTAC 1095  
QY 181 CCAGGGTGCAATACCTA 198  
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Db 1096 CCAGGGTGCAATACCTA 1113

RESULT 2  
US-09-974-592-9  
; Sequence 9, Application US/09974592  
; Patent No. US20020120121A1  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G  
; APPLICANT: Mackenzie, Alexander E  
; APPLICANT: Liston, Peter  
; APPLICANT: Baird, Stephen  
; APPLICANT: Tsang, Benjamin K  
; APPLICANT: Pratt, Christine  
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND  
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE  
; TITLE OF INVENTION: DISEASE  
; FILE REFERENCE: 07891/009004  
; CURRENT APPLICATION NUMBER: US/09/974,592  
; CURRENT FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: US 09/617,053  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 08/800,929  
; PRIOR FILING DATE: 1997-02-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-974-592-9

Query Match 98.4%; Score 194.8; DB 10; Length 2691;  
Best Local Similarity 99.0%; Pred. No. 3.7e-58;  
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATTAAGTGAAGTCTTCCACTGTGA 120  
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Db 1521 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATTAAGTGAAGTCTTCCACTGTGA 1580  
QY 121 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGGACCCAGCATGCTAAAGTGCTAC 180  
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Db 1581 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGGACCCAGCATGCTAAAGTGCTAC 1640  
QY 181 CCAGGGTGCAATACCTA 198  
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Db 1641 CCAGGGTGCAATACCTA 1658

RESULT 3  
US-09-964-899-38  
; Sequence 38, Application US/09964899  
; Patent No. US2002017446A1  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Dalia et al.  
; TITLE OF INVENTION: Identification of Genes Involved in  
; TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster  
; FILE REFERENCE: 4-31612 A  
; CURRENT APPLICATION NUMBER: US/09/964,899  
; CURRENT FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: 60/236,893  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/298,309

; PRIOR FILING DATE: 2001-06-14  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 38  
; LENGTH: 2404  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-09-964-899-38

Query Match 87.4%; Score 173; DB 9; Length 2404;  
Best Local Similarity 92.4%; Pred. No. 1.6e-50;  
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
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Db 827 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAGTAAAGGAGCAGCTT 886  
QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATTAAGTGAAGTCTTCCACTGTGA 120  
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Db 887 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATTAAGTGAAGTCTTCCACTGTGA 946  
QY 121 GGAGGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGGACCCAGCATGCTAAAGTGCTAC 180  
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Db 947 GGAGGGCTAAGTGAAGCCCAAGTGAAGACCCCTGGGACCCAGCATGCTAAAGTGCTAT 1006  
QY 181 CCAGGGTGCAATACCT 197  
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Db 1007 CCAGGGTGCAATACCT 1023

RESULT 4  
US-09-201-936-3  
; Sequence 3, Application US/09201936  
; Publication No. US20020187946A1  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: Mackenzie, Alexander E.  
; APPLICANT: Baird, Stephen  
; APPLICANT: Liston, Peter  
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS  
; FILE REFERENCE: 07891/003003  
; CURRENT APPLICATION NUMBER: US/09/201,936  
; CURRENT FILING DATE: 1998-12-01  
; EARLIER APPLICATION NUMBER: 09/011,356  
; EARLIER FILING DATE: 1998-02-04  
; EARLIER APPLICATION NUMBER: PCT/IB96/01022  
; EARLIER FILING DATE: 1996-08-05  
; EARLIER APPLICATION NUMBER: 08/376,956  
; EARLIER FILING DATE: 1995-12-22  
; EARLIER APPLICATION NUMBER: 08/511,485  
; EARLIER FILING DATE: 1995-08-04  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 2540  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (2540)...(2540)  
; OTHER INFORMATION: N may be any nucleotide  
US-09-201-936-3

Query Match 87.4%; Score 173; DB 9; Length 2540;  
Best Local Similarity 92.4%; Pred. No. 1.6e-50;  
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;  
QY 1 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAGTAAAGGAGCAGCTT 60  
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Db 826 TATGAAGCAGCGATCGTTACTTTTGGACATGGATATCTCAGTTAAGTAAAGGAGCAGCTT 885  
QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGCGGATTAAGTGAAGTCTTCCACTGTGA 120

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Db 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGTCTTCACTGTGGA 945
QY 121 GGAGGCTCAGGATTTGAAGCCAAAGTGAAGACCCCTGGGACCAAGCATGCTTAAGTGTAC 180
Db 946 GGAGGGCTAACTGATTGAAGCCCAAGTGAAGACCCCTGGGAAACAACATGCTTAATGGTAT 1005
QY 181 CCAGGGTGCAAAATACCT 197
Db 1006 CCAGGGTGCAAAATATCT 1022

RESULT 5
US-09-974-592-3
; Sequence 3, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: 4623
; OTHER INFORMATION: n can be any nucleotide
; NAME/KEY: variation
; LOCATION: 4622
; OTHER INFORMATION: n can be any nucleotide
; US-09-974-592-3

Query Match 87.4%; Score 173; DB 10; Length 5232;
Best Local Similarity 92.4%; Pred. No. 2.2e-50;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATGCTTTACTTTTGGACATGGATATACCTAGTAAAGTGTCTTCACTGTGGA 60
Db 886 TATGAAGCAGCGATGCTTTACTTTTGGACATGGATATACCTAGTAAAGTGTCTTCACTGTGGA 885
QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCCAAAGTGAAGACCCCTGGGACCAAGCATGCTT 120
Db 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCCCAAGTGAAGACCCCTGGGAAACAACATGCTT 945
QY 121 GGAGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGGACCAAGCATGCTTAAGTGTAC 180
Db 946 GGAGGGCTAACTGATTGAAGCCCAAGTGAAGACCCCTGGGAAACAACATGCTTAATGGTAT 1005
QY 181 CCAGGGTGCAAAATACCT 197
Db 1006 CCAGGGTGCAAAATATCT 1022

RESULT 6
US-10-095-407-16/c
; Sequence 16, Application US/10095407
; Patent No. US20020164330A1
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; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/10/095,407
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/091,650
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/054,646
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 152331
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
; US-10-095-407-16

Query Match 67.9%; Score 134.4; DB 9; Length 152331;
Best Local Similarity 83.2%; Pred. No. 3.6e-36;
Matches 164; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

QY 1 TATGAAGCAGCGATGCTTTACTTTTGGACATGGATATACCTAGTAAAGTGTCTTCACTGTGGA 60
Db 3298 TATGAAGCAGCGATGCTTTACTTTTGGATGTGGATATATTCAGTAAAGGAGCAGCTT 3239
QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGCCAAAGTGAAGTGTCTTCCACTGTGGA 120
Db 3238 TCAAGAGCTGGATTTATGCTTTAGGTGAAGTGTATAAAGTGTCTTTCACCTGTGGA 3179
QY 121 GGAGGCTCAGGATTTGAAGCCCAAGTGAAGACCCCTGGGACCAAGCATGCTTAAGTGTAC 180
Db 3178 GGGGGCTAACTGATTGGGAACCCACCAGAA-AACCTTGGGACCAACATAATAATGGGAT 3120
QY 181 CCAGGGTGCAAAATACCT 197
Db 3119 CCAGGTGTAAATATCT 3103

RESULT 7
US-10-095-407-17
; Sequence 17, Application US/10095407
; Patent No. US20020164330A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/10/095,407
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/091,650
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/054,646
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 176373
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C or G
; US-10-095-407-17

Query Match 55.4%; Score 109.6; DB 9; Length 176373;
Best Local Similarity 86.4%; Pred. No. 2e-27;
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; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1635
; LENGTH: 3076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1635

Query Match
Best Local Similarity 38.4%; Score 76; DB 10; Length 3076;
Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 42 AGTTAAACGAGGAGCAGCTTGCAGAGCTGCGATTTTATGCTTAGGTGAAGCGGATAAAGT 101
Db 1534 AGTTAACTCTGAGCAGCTTGCAGAGCTGCGGTTTATATGCTTAGGTGAAGCGGATAAAGT 1593

Qy 102 GAAGTGTCTTCCACTGTGCGAGAGGCTTCACGGATTGCGATTTTATGCTTAGGTGAAGCGGATAAAGT 197
Db 1594 CAATGCTTTTGTGTGATGCTGAGTGCAGGTGCTGGGAATCTGGAGATGATCCATGGGT 1653

Qy 162 CCAGCATGCTAAAGTCTACCCAGGCTGCAAGGTCGAATACCT 197
Db 1654 TCAACATGCCAAGTGTTCACAGGTGTGAGTACTT 1699

RESULT 11
US-09-974-592-5
; Sequence 5, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 6669
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (3677)...(3951)
; OTHER INFORMATION: n can be any nucleotide
US-09-974-592-5

Query Match
Best Local Similarity 38.4%; Score 76; DB 10; Length 6669;
Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 42 AGTTAAACGAGGAGCAGCTTGCAGAGCTGCGATTTTATGCTTAGGTGAAGCGGATAAAGT 101
Db 1534 AGTTAACTCTGAGCAGCTTGCAGAGCTGCGGTTTATATGCTTAGGTGAAGCGGATAAAGT 1593

; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1635
; LENGTH: 3076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1635

Query Match
Best Local Similarity 38.4%; Score 76; DB 10; Length 3076;
Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 42 AGTTAAACGAGGAGCAGCTTGCAGAGCTGCGATTTTATGCTTAGGTGAAGCGGATAAAGT 101
Db 1534 AGTTAACTCTGAGCAGCTTGCAGAGCTGCGGTTTATATGCTTAGGTGAAGCGGATAAAGT 1593

Qy 102 GAAGTGTCTTCCACTGTGCGAGAGGCTTCACGGATTGCGATTTTATGCTTAGGTGAAGCGGATAAAGT 197
Db 1594 CAATGCTTTTGTGTGATGCTGAGTGCAGGTGCTGGGAATCTGGAGATGATCCATGGGT 1653

Qy 162 CCAGCATGCTAAAGTCTACCCAGGCTGCAAGGTCGAATACCT 197
Db 1654 TCAACATGCCAAGTGTTCACAGGTGTGAGTACTT 1699

RESULT 12
US-09-201-936-39
; Sequence 39, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 2450
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-39

Query Match
Best Local Similarity 34.3%; Score 68; DB 9; Length 2450;
Matches 101; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

Qy 42 AGTTAAACGAGGAGCAGCTTGCAGAGCTGCGATTTTATGCTTAGGTGAAGCGGATAAAGT 101
Db 965 AGTTCAATCCAGGAACCTGCAAGTGGCGGCTTTATATACAGCACACAGTGTATGT 1024

Qy 102 GAAGTGTCTTCCACTGTGCGAGAGGCTTCACGGATTGCAAGCCTGGAAGCCCTGGGA 161
Db 1025 CAAGTGTATGCTGTGATGGTGGCTGAGGTGCTGGGAATCTGGAGATGACCCCTGGGT 1084

Qy 162 CCAGCATGCTAAAGTCTACCCAGGCTGCAATACCT 197
Db 1085 GGAACATGCCAAGTGTTCACAGGTGTGAGTACTT 1120

RESULT 13
US-09-974-592-11
; Sequence 11, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009004

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; CURRENT APPLICATION NUMBER: US/09/974,592  
; CURRENT FILING DATE: 2001-10-09  
; PRIOR APPLICATION NUMBER: US 09/617,053  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 08/800,929  
; PRIOR FILING DATE: 1997-02-13  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11  
; LENGTH: 2676  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-974-592-11

Query Match 34.3%; Score 68; DB 10; Length 2676;  
Best Local Similarity 64.7%; Pred. No. 1.2e-13;  
Matches 101; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 42 AGTTACAAGGACGCTGCGAAGAGCTGGATTTTATGCTTTAGGTGAAGCGGATAAAGT 101  
DB 1106 AGTTCAATCCAGGACTTGCAGTCCGGCTTTATTATACAGACACAGTGATGATGT 1165  
QY 102 GAAGTCTTCCACTGTTGGAGGAGGCTCAGGATGGAGGCAAGTGAAGACCCCTGGGA 161  
DB 1166 CAAAGTCTTCTGTGTGTTGGCTGAGGTGGGAATCTGGAGATGACCCCTGGGT 1225  
QY 162 CCAGCATGCTAAGTCTACCCAGGCTGCAAAATACCT 197  
DB 1226 GGAACATGCCAAGTGTTCCTCAAGTGTGAGTACTT 1261

## RESULT 14

US-09-201-936-7  
; Sequence 7, Application US/09201936  
; Publication No. US20020187946A1  
; GENERAL INFORMATION:  
; APPLICANT: Korneluk, Robert G.  
; APPLICANT: Mackenzie, Alexander E.  
; APPLICANT: Baird, Stephen  
; APPLICANT: Liston, Peter  
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,  
; FILE OF INVENTION: PROBES, AND DETECTION METHODS  
; FILE REFERENCE: 07891/003003  
; CURRENT APPLICATION NUMBER: US/09/201,936  
; CURRENT FILING DATE: 1998-12-01  
; EARLIER APPLICATION NUMBER: 09/011,356  
; EARLIER FILING DATE: 1998-02-04  
; EARLIER APPLICATION NUMBER: PCT/IB96/01022  
; EARLIER FILING DATE: 1996-08-05  
; EARLIER APPLICATION NUMBER: 08/576,956  
; EARLIER FILING DATE: 1995-12-22  
; EARLIER APPLICATION NUMBER: 08/511,485  
; EARLIER FILING DATE: 1995-08-04  
; NUMBER OF SEQ ID NOS: 45  
; SOFTWARE: FastSeq for Windows Version: 3.0  
; SEQ ID NO 7  
; LENGTH: 2580  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: variation  
; LOCATION: (2412)...(2412)  
; OTHER INFORMATION: N may be any nucleotide  
US-09-201-936-7

Query Match 33.2%; Score 65.8; DB 9; Length 2580;  
Best Local Similarity 60.2%; Pred. No. 7e-13;  
Matches 109; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 17 TTATGTTTGGACATGATATACCTCAGTTAACAAGGAGGAGCTTGAAGAGCTGGATTTT 76  
DB 1064 TTATGTTTGGACATGATATACCTCAGTTAACAAGGAGGAGCTTGAAGAGCTGGATTTT 1123

QY 77 ATGCTTTAGGTGAAGCGGATAAAGTCAAGTGGCTTCCACTGTGGAGAGGGCTCAGGATT 136  
DB 1124 ATTATGTGGTGGTCCATGATGATGTCAAATGCTTTGGTTGATGCTGGCTTTGAGTGT 1183  
QY 137 GGAAGCCCAAGTGAAGACCCCTGGGACCATGCTAAAGTGTCTACCCAGGCTCAAAATACC 196  
DB 1184 GGAATCTGGAGATGATCCATGGGTAGAACATGCCAAGTGGTTTCCAAAGGTGAGTCT 1243  
QY 197 T 197  
DB 1244 T 1244

## RESULT 15

US-09-880-107-3354  
; Sequence 3354, Application US/09880107  
; Patent No. US20020142981A1  
; GENERAL INFORMATION:  
; APPLICANT: Horne, Darci T.  
; APPLICANT: Vockley, Joseph G.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Gene Logic, Inc.  
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer  
; FILE REFERENCE: 44921-5028-WO  
; CURRENT APPLICATION NUMBER: US/09/880,107  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: US 60/211,379  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: US 60/237,054  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 3950  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3354  
; LENGTH: 3532  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U37547  
US-09-880-107-3354

Query Match 33.2%; Score 65.8; DB 10; Length 3532;  
Best Local Similarity 60.2%; Pred. No. 8.1e-13;  
Matches 109; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 17 TTACTTTTGAACATGATATACCTCAGTTAACAAGGAGGAGCTTGAAGAGCTGGATTTT 76  
DB 1986 TTATGTTTGGTCCATGATGATGTCAAATGCTTTGTTGATGGTGGCTTGAAGTGT 2045  
QY 77 ATGCTTTAGGTGAAGCGGATAAAGTGAAGTGGCTTCCACTGTGGAGAGGGCTCAGGATT 136  
DB 2046 ATTATGTGGTCCATGATGATGTCAAATGCTTTGTTGATGGTGGCTTGAAGTGT 2105  
QY 137 GGAAGCCCAAGTGAAGACCCCTGGGACCATGCTAAAGTGTCTACCCAGGCTCAAAATACC 196  
DB 2106 GGAATCTGGAGATGATCCATGGGTAGAACATGCCAAGTGGTTTCCAAAGGTGAGTCT 2165  
QY 197 T 197  
DB 2166 T 2166

Search completed: April 19, 2003, 03:05:22  
Job time : 148 secs

GenCore version 5.1.4\_p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 19, 2003, 01:38:31 ; Search time 1057 Seconds  
(without alignments)  
3033.781 Million cell updates/sec

Title: US-09-654-743-51

Perfect score: 198

Sequence: 1 tatgaagcagcagtcgttac.....accacgggtgcaataaccta 198

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estor:\*

5: em\_estov:\*

6: em\_estpi:\*

7: em\_estro:\*

8: em\_htc:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: gb\_gss:\*

18: em\_gss\_hum:\*

19: em\_gss\_inv:\*

20: em\_gss\_pln:\*

21: em\_gss\_vrt:\*

22: em\_gss\_fun:\*

23: em\_gss\_mam:\*

24: em\_gss\_mus:\*

25: em\_gss\_other:\*

26: em\_gss\_pro:\*

27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	168	84.8	628	9	AI573382	AI573382 mn83e12.x
C 2	108	54.5	617	10	BB663325	BB663325 BB663325
C 3	103.4	52.2	504	10	BB650856	BB650856 BB650856
C 4	100.8	50.9	318	12	BF659610	BF659610 uz88e12.x
C 5	98	49.5	566	13	BM220130	BM220130 C0935E08-
C 6	98	49.5	584	14	BQ552032	BQ552032 H4013A06-

7	92.2	46.6	1177	14	BM805359
8	90.2	45.6	536	9	AUI23207
9	84.2	42.5	716	10	AV706807
10	76	38.4	341	10	AW375598
11	76	38.4	354	10	AW375594
12	76	38.4	402	10	AW846507
13	76	38.4	531	10	AW375599
14	76	38.4	532	10	AW846525
15	76	38.4	546	10	AW846421
16	76	38.4	571	10	AW375649
17	76	38.4	582	10	AW846337
18	76	38.4	590	10	BE268377
19	76	38.4	621	10	AW375648
20	76	38.4	680	10	AW375625
21	76	38.4	886	14	BQ652590
22	75.2	38.0	269	10	BE506790
23	69.2	34.9	567	13	BI961039
24	68.4	34.5	420	17	AQ011995
25	68	34.3	323	12	BE847058
26	68	34.3	385	12	BE851680
27	66	33.3	557	9	AA197349
28	66	33.3	673	13	BJ045197
29	65.8	33.2	441	13	BM312708
30	65.8	33.2	563	9	AA702174
31	65.8	33.2	652	10	AV704923
32	65.8	33.2	851	13	BI253303
33	65.8	33.2	896	14	BQ439248
34	65.4	33.0	354	9	AA354707
35	64.2	32.4	506	13	BM126304
36	63.8	32.2	889	14	BQ720079
37	62.6	31.6	780	13	BI771720
38	62.4	31.5	302	14	R83677
39	62.4	31.5	512	13	BI326908
40	62.4	31.5	584	10	AW375608
41	62.4	31.5	645	10	AW375611
42	61.2	30.9	620	13	BM494270
43	61	30.8	288	12	BF016190
44	60.6	30.6	395	9	AI552965
45	59.6	30.1	423	12	BF325539

## ALIGNMENTS

## RESULT 1

AI573382/c

LOCUS

DEFINITION

AI573382

AI573382

AI573382.1

GI:4536756

EST.

house mouse.

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

1 (bases 1 to 628)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person

, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter

, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCand, R.,

Waterston, R. and Wilson, R.

The WashU-NCI Mouse EST Project 1999

Unpublished (1999)

Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LINL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Possible reversed clone: similarity on wrong strand

AI573382 628 bp mRNA linear EST 16-APR-1999  
mn83e12.x1 Stragatene mouse Tcell 937311 Mus musculus cDNA clone  
IMAGE:550702 3' similar to TR:Q60989 Q60989 MIHA. ; mRNA sequence.

AI573382.1 GI:4536756  
EST.  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 628)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,  
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person  
, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter  
, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCand, R.,  
Waterston, R. and Wilson, R.

The WashU-NCI Mouse EST Project 1999  
Unpublished (1999)

Contact: Marra M/WashU-NCI Mouse EST Project 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800  
Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LINL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Possible reversed clone: similarity on wrong strand

High quality sequence stop: 440.

prepare full-length cDNA libraries for rapid discovery of new genes. *Genome Res.* 10 (10), 1617-1630 (2000)

wagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Toneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. *Genome Res.* 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y., and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)

Kondo, S., Shinozawa, A., Saito, T., Kiyosawa, H., Yamanaka, J., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. *Mamm. Genome.* 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES	source
e mouse tissues.	
Location/Qualifiers	
1. .617	

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="D930039G22"
/clone_lib="RIKEN full-length enriched, 15 days embryo
head"
/sex="mixed"
/tissue_type="head"
/dev_stage="15 days embryo"
/lab_host="DH10B"
/note="site_1: Salt; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGGATCCGAGAGCTCTTTTITTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5',
GAGAGAGAGATCTCGAGTAAATTAATATCCCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda

```

BASE COUNT	198 a	121 c	160 g	137 t	1 others
ORIGIN					
Query Match	54.5%;	Score 108;	DB 10;	Length 617;	
Best Local Similarity	91.9%;	Pred. No. 4.8e-24;			
Matches 114; Conservative	0;	Mismatches 10;	Indels	0;	Gaps 0;
QY	75	TTATGCTTTAGTGAAGCGGATAAAGTGAAGTGCTTCACACTGTGGAGGAGGGGCTCACGGA	134		
Dbb	108	TGACACCTTAAGSTGAAGCGGATAAAGTGAAGTGCTTTCACTGTGGAGGAGGGGCTCACGGA	167		
QY	135	TTGGAAGCCCAAGTGAAGACCCTTGGGACCAGCATGCTAAAGTGCTACCCAGGGGTGCCAAAATA	194		
Dbb	168	TTGGAAGCCCAAGTGAAGACCCTTGGGAACAGCATGCGAAAGTGATCCCAGGGGTGCCAAAATA	227		
QY	195	CCTA	198		
Dbb	228	CCTA	231		
RESULT 3					
BB650856					
LOCUS	BB650856	504 bp	mRNA	linear	FST 26-OCT-2001

```

FEATURES
source
1. 628
Location/Qualifiers
/db_xref="taxon:10090"
/clone_lib="Stratagene mouse Tcell 937311"
/tissue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: blood; Vector: pBluescript SK-; Site:1: EcoRI; Site:2: XhoI; Cloned unidirectionally. Primer: Oligo dt. M30 CD4+ cells. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCACACAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'."
163 a 137 C 115 g 211 t 2 others
BASE COUNT
ORIGIN

```

Query Match	84.8%;	Score 168;	DB 9;	Length 628;
Best Local Similarity	93.4%;	Pred. No. 1.7e-43;		
Matches 185;	Conservative	0;	Mismatches 12;	Indels 1;
QY	1	TATGAAGCAGCGATCGTTACTTTTGGAAACATGGGATATACTCAGTTTAAACAAGGAGCAGCTT	60	
Db	604	TATGAAGCAGCGATCGTTACTTTTGGNACATGGACATCCTCAGTTTACAAAGGAGCAGCTT	545	
QY	61	GCAAGAGCTGGAATTTATGCTTTAGCTGAAGGCGGATAAAGTGAAGTGCCTTCCAAGTGTGA	120	
Db	544	GCAAGAGCT-GAATTTATGCTTTAGTGAAGGCGGATAAAGTGAAGTGCCTTCCAAGTGTGA	486	
QY	121	GGAGGCGCTCACGGATTGGGAAGCCAAAGTGAAGACCCCTGGGACACAGCATGCTAAGTGCCTAC	180	
Db	485	GGAGGCGCTCACGGATTGGGAAGCCAAAGTGAAGACCCCTGGGAAACAGCATGCGAAGTGCCTAC	426	
QY	181	CCAGGCTGCAAAATACCTA	198	
Db	425	NCAGGCTGCAAAATACCTA	408	

RESULT 2	BB6633325	617 bp	linear	EST 26-OCT-2001
LOCUS	BB6633325	RIKEN full-length enriched, 15 days embryo head Mus		
DEFINITION	musculus cdna clone D930039G22 5', mRNA sequence.			
ACCESSION	BB6633325			
VERSION	BB6633325.1	GI:16497079		
KEYWORDS	EST.			
SOURCE	house mouse			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Euthera; Rodentia; Sclurognathi; Muridae; Murinae; Mus.			
	1 (bases 1 to 617)			
	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,			
	Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda			
	M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,H., Kouda			
	Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki			
	D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,			
	Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,			
	Muramatsu,M. and Hayashizaki,Y.			
	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)			
	Unpublished (2001)			
	Contact: Yoshihide Hayashizaki			
	Laboratory for Genome Exploration Research Group, RIKEN Genomic			
	Sciences Center(GSC), Yokohama Institute			
	The Institute of Physical and Chemical Research (RIKEN)			
	1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan			
	Tel: 81-45-503-9222			
	Fax: 81-45-503-9216			
	Email: genome-res@gsic.riken.go.jp,			
	URL:http://genome.gsc.riken.go.jp/			
	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh			
	M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.			
	Normalization and subtraction of cap-trapper-selected cDNAs to			
TITLE	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Yoshihide Hayashizaki			
	Laboratory for Genome Exploration Research Group, RIKEN Genomic			
	Sciences Center(GSC), Yokohama Institute			
	The Institute of Physical and Chemical Research (RIKEN)			
	1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan			
	Tel: 81-45-503-9222			
	Fax: 81-45-503-9216			
	Email: genome-res@gsic.riken.go.jp,			
	URL:http://genome.gsc.riken.go.jp/			
	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh			
	M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.			
	Normalization and subtraction of cap-trapper-selected cDNAs to			



Best Local Similarity 93.8%; Pred. No. 6.7e-22;  
Matches 105; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 53 ACACCTTCACAGAGCTGATTTATGCTTAGGTGAAGCGCATAAAGTGAAGTCTTCC 112  
DB 317 ACACCTTCACAGAGCTGATTTATGCTTAGGTGAAGCGCATAAAGTGAAGTCTTCC 258  
QY 113 ACTGGGAGGAGGCTCAGGATTCGAGCCCAAGTGAAGACCCCTGGGACCA 164  
DB 257 ACTGGGAGGAGGCTCAGGATTCGAGCCCAAGTGAAGACCCCTGGGACCA 206

RESULT 5  
BM220130/c 566 bp mRNA linear EST 31-JAN-2002  
LOCUS C0935E08-3 NIA Mouse 12.5-dpc Male Genital Ridge/Mesonephros cDNA  
DEFINITION Library (Long) Mus musculus cDNA clone C0935E08 3', mRNA sequence.  
ACCESSION BM220130  
VERSION BM220130.1 GI:17780130  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 566)  
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Pantano, S., Luo, A.  
and Ko, M.S.H.

TITLE Systematic Analyses of NIA Mouse 12.5-dpc Male Genital  
JOURNAL Ridge/Mesonephros cDNA Library (Long)  
COMMENT unpublished (2001)  
Contact: Dawood B. Dudekula  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA  
Email: cdna@igsun.grc.nia.nih.gov  
Plate: C0935 row: E column: 08  
Seq primer: -21M13 Forward  
High quality sequence stop: 566  
POLYA=Yes.

FEATURES Location/Qualifiers  
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/db\_xref="taxon:10090"  
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Ridge/Mesonephros cDNA Library (Long)"  
/sex="Male"  
/tissue\_type="Male genital ridge/mesonephros"  
/dev\_stage="12.5-dpc"  
/lab\_host="DH10B"  
/note="Vector: pSPORT1 (Invitrogen); Site\_1: SalI; Site\_2:  
NotI; Mouse cDNA project by the Laboratory of Genetics,  
National Institute on Aging (NIA), Intramural Research  
Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is  
a long-transcript enriched cDNA library (Ref. Genome Res.  
11: 1553-1558 (2001). [PMID: 11544199]). Double-stranded  
cDNAs were synthesized with an Oligo(dT) primer  
[Invitrogen]:  
5'-pCAGTAGTCTAGATCGGCGGCCCTTTTCTTTT-3' from  
1.8 ug of total RNA, treated with T4 DNA polymerase, and  
purified by ethanol-precipitation. The cDNAs were ligated  
to lOne-linker LL-Sal4, purified by phenol/chloroform, and  
separated from free linkers by Centricon 100. Then, the  
cDNAs were amplified by long-range high fidelity PCR using  
Ex Taq polymerase (Takara) with a primer Sal4-S. The  
products were purified by phenol/chloroform and Centricon  
100. The cDNAs were digested with SalI and NotI enzymes  
and cloned into SalI/NotI site of pSPORT1 plasmid vector.  
The DH10B E. coli host was transformed with the ligation  
mixture by the standard chemical method. The average  
insert size is about 2.4 kb. The library was constructed

BASE COUNT 183 a 123 c 84 g 176 t  
ORIGIN by Yulan Piao (NIA)."

Query Match 49.5%; Score 98; DB 13; Length 566;  
Best Local Similarity 95.3%; Pred. No. 7.9e-21;  
Matches 101; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 82 TTAGTGAAGCGCATAAAGTGAAGTCTTCCACTGTGGAGGAGGCTCAGGATTGGAAG 141  
DB 260 TTAGTGAAGCGCATAAAGTGAAGTCTTCCACTGTGGAGGAGGCTCAGGATTGGAAG 201

QY 142 CCAAGTGAAGACCCCTGGGACCAAGTGAAGTCTTCCACTGTGGAGGAGGCTCAGGATTGGAAG 187  
DB 200 CCAAGTGAAGACCCCTGGGACCAAGTGAAGTCTTCCACTGTGGAGGAGGCTCAGGATTGGAAG 155

RESULT 6  
BQ552032/c 584 bp mRNA linear EST 20-JUN-2002  
LOCUS H4013A06-3 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone  
DEFINITION H4013A06 3', mRNA sequence.  
ACCESSION BQ552032  
VERSION BQ552032.1 GI:21452918  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 584)  
VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., Carter, M.G., Martin,  
P.R., Staggs, C.A., Bassey, U., Aliba, K., Hamatani, T., Kargul, G.J.,  
Luo, A.G. and Ko, M.S.H.  
Assembly, verification, and initial annotation of NIA 7.4K mouse  
cDNA clone set  
Unpublished (2002)  
Other ESTs: H4013A06-5  
Contact: Yong Qian  
Laboratory of Genetics  
National Institute on Aging/National Institutes of Health  
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA  
Email: cdna@igsun.grc.nia.nih.gov  
This clone set has been freely distributed to the community. Please  
visit http://igsun.grc.nia.nih.gov/cDNA/NIA\_7.4k.html for details.  
Plate: H4013 row: A column: 06  
Seq primer: -21M13 Forward  
High quality sequence stop: 584  
POLYA=Yes.

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/sex="mixed"  
/dev\_stage="mixed"  
/lab\_host="DH10B"  
/note="Vector: pSPORT1; Site\_1: SalI; Site\_2: NotI; This  
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than 20 cDNA libraries."  
BASE COUNT 189 a 125 c 86 g 184 t  
ORIGIN

Query Match 49.5%; Score 98; DB 14; Length 584;  
Best Local Similarity 95.3%; Pred. No. 8.1e-21;  
Matches 101; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 82 TTAGTGAAGCGCATAAAGTGAAGTCTTCCACTGTGGAGGAGGCTCAGGATTGGAAG 141  
DB 260 TTAGTGAAGCGCATAAAGTGAAGTCTTCCACTGTGGAGGAGGCTCAGGATTGGAAG 201

## FEATURES

LOCATION/QUALITY

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/clone_lib="ADB"
/tissue_type="Adrenal gland"
/dev_stage="Adult"
/lab_host="SOLR"
/note="vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 207 a 148 c 193 g 163 t 5 others
ORIGIN

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Best Local Similarity 84.1%; Pred. No. 2.8e-16;
Matches 95; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 85 GGTGAAGCGGATAAGTGAAGTGTCTTCACTGTGGAGAGGGCTCACGGATTGGAAGCCA 144
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Db 156 GGTGAAGGTATAAGTAAAGTGTCTTCACTGTGGAGAGGGCTTAAGTGTGAAGCCC 215
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QY 145 AGTGAAGACCCCTGGGACCAAGCATGCTAAAGTGTACCCAGGGTGCAATACCT 197
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Db 216 AGTGAAGACCCCTGGGACCAAGCATGCTAAATGGTATCCAGGGTAAGAAGTACT 268
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RESULT 10
AW375598
LOCUS QV0-CT0179-300999-024-f08 CT0179 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION AW375598
VERSION AW375598.1 GI:6880161
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 341)
AUTHORS HCSP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-QV0&st2-QV0-CT0179-
300999-024-f08&t3-1999-09-30&t4-1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 341.
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Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0179"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 91 a 70 c 83 g 97 t
ORIGIN

Query Match 38.4%; Score 76; DB 10; Length 341;
Best Local Similarity 67.9%; Pred. No. 7.9e-14;
Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 42 AGTTAAACAGGACGAGCTTGAAGAGCTGGATTTTATGCTTTAGTGAGCGGATAAAGT 101
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Db 93 AGTTAACTCTGAGCAGCTTGAAGTGGGGTTTATATATGTTGGGTACAGTGATGATCT 152
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QY 102 GAAGTGCTTCCACTGTGGAGGAGGCTCACGGATTGGAGCCCAAGTGAAGACCCCTGGGA 161
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Db 153 CAAATGCTTTGCTGTGATGGTGGACTCAGGTGTGGGAATCTGGAGATGATCCATGGCT 212
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Best Local Similarity 67.9%; Pred. No. 7.7e-14;
Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 42 AGTTAAACAGGACGAGCTTGAAGAGCTGGATTTTATGCTTTAGTGAGCGGATAAAGT 101
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Db 80 AGTTAACTCTGAGCAGCTTGAAGTGGGGTTTATATATGTTGGGTACAGTGATGATCT 139
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QY 102 GAAGTGCTTCCACTGTGGAGGAGGCTCACGGATTGGAGCCCAAGTGAAGACCCCTGGGA 161
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 140 CAAATGCTTTGCTGTGATGGTGGACTCAGGTGTGGGAATCTGGAGATGATCCATGGCT 199
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QY 162 CCAGCATGCTAAAGTGTACCCAGGGTGCAATACCT 197
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Db 200 TCACATGCCAAGTGGTTCACAGGTGTGAGTACTT 235
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RESULT 11
AW375594
LOCUS QV0-CT0179-300999-024-d06 CT0179 Homo sapiens cDNA, mRNA sequence.
DEFINITION
ACCESSION AW375594
VERSION AW375594.1 GI:6880157
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 354)
AUTHORS HCSP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-QV0&st2-QV0-CT0179-
300999-024-d06&t3-1999-09-30&t4-1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence stop: 354.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CT0179"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 96 a 73 c 86 g 99 t
ORIGIN

Query Match 38.4%; Score 76; DB 10; Length 354;
Best Local Similarity 67.9%; Pred. No. 7.9e-14;
Matches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 42 AGTTAAACAGGACGAGCTTGAAGAGCTGGATTTTATGCTTTAGTGAGCGGATAAAGT 101
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 93 AGTTAACTCTGAGCAGCTTGAAGTGGGGTTTATATATGTTGGGTACAGTGATGATCT 152
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QY 102 GAAGTGCTTCCACTGTGGAGGAGGCTCACGGATTGGAGCCCAAGTGAAGACCCCTGGGA 161
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Db 153 CAAATGCTTTGCTGTGATGGTGGACTCAGGTGTGGGAATCTGGAGATGATCCATGGCT 212
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```





SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 532)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.J.

Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

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Ludwig Institute for Cancer Research  
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Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=4t2-QV0-CT0179-070  
300-143-0046t3-2000-03-07&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 4

High quality sequence stop: 531.

Location/Qualifiers

1. .532

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="CT0179"

/dev\_stage="Adult"

/note="Organ: colon; Vector: puc18; Site\_1: SmaI; Site\_2:

SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No. 196

,716 - Ludwig Institute for Cancer Research) profiles

into the PUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

BASE COUNT 160 a 107 c 122 g 143 t

ORIGIN

Query Match

Best Local Similarity 38.4%; Score 76; DB 10; Length 532;

Mismatches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 42 AGTTACAGGAGCAGCTTGCAGAGCTGGATTTTATGCTTTAGTGAAGCGGATAAGT 101

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QY 162 CCAGCATGCTAAGTGTACCCAGGCTGCAAACTCT 197

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Db 216 TCAACATGCCAAGTGGTTTCCAAAGGTGTGAGTACTT 251

RESULT 15

AW846421

LOCUS

DEFINITION

AW846421

ACCESSION

AW846421.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS

1 (bases 1 to 546)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,

Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare

M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and

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This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=4t2-QV0-CT0179-070

300-143-0046t3-2000-03-07&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 6

High quality sequence stop: 546.

Location/Qualifiers

1. .546

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="CT0179"

/dev\_stage="Adult"

/note="Organ: colon; Vector: puc18; Site\_1: SmaI; Site\_2:

SmaI; A mini-library was made by cloning products derived

from ORESTES PCR (U.S. Letters Patent application No. 196

,716 - Ludwig Institute for Cancer Research) profiles

into the PUC 18 vector. Reverse transcription of tissue

mRNA and cDNA amplification were performed under low

stringency conditions."

BASE COUNT 169 a 106 c 123 g 148 t

ORIGIN

Query Match

Best Local Similarity 38.4%; Score 76; DB 10; Length 546;

Mismatches 106; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 42 AGTTACAGGAGCAGCTTGCAGAGCTGGATTTTATGCTTTAGTGAAGCGGATAAGT 101

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Db 121 AGTTAATCTGAGCAGCTTGCAGAGCTGGGTTTATTTATGTTGGTACAGTATGATGT 180

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Db 241 TCAACATGCCAAGTGGTTTCCAAAGGTGTGAGTACTT 276

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Job time : 1062 secs



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